



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 154940

TO: Bao-Qun Li
Location: rem/3d24/3c18
Art Unit: 1648
Monday, June 06, 2005

Case Serial Number: 10/649480

From: Alex Waclawiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

1574940

From: Li, Bao-Qun
Sent: Tuesday, May 31, 2005 1:52 PM
To: STIC-Biotech/ChemLib
Subject: 10,649,480

Please do the sequence homology and interference search for SEQ ID NO: 7, and 2.

Bao Qun Li M.D
TC 1600
Art Unit 1648
Tel. 517-272-0904
REM, 3C18
Rm. 3D24

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Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CM1-6A02 Tel. 308-4491

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: 6-6-05
Date Completed: 6-6-05
Searcher Prep/Rev. Time: _____
Online Time: 14

Type of Search

NA#: _____ AA#: 2
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:37 ; Search time 109.561 Seconds
(without alignments) 497.744 Million cell updates

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPPGNYKKPKLLYCSNG.....PRTHYGQKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000
Maximum DB seq length: 200000000

..... For the

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A Geneseq 16Dec04: *

```
1: _ geneseqp1980s:*
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2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	762	100.0	141	2	AAR10527	Human aci
2	762	100.0	141	5	Aau76945	Human aci
3	762	100.0	141	5	Aau76945	Protein o
4	762	100.0	141	8	ADO19992	Human aci
5	762	100.0	141	8	ADO55206	Human aci
6	757	99.3	140	1	AAR05789	Human aFG
7	757	99.3	140	1	AAP70395	Sequence
8	757	99.3	140	1	AAP90068	Human aci
9	757	99.3	140	2	AAR25914	Human aci
10	757	99.3	140	2	AAR34497	Human aci
11	757	99.3	140	2	AAR74647	Human rec
12	757	99.3	154	2	Aaw04806	Human aci
13	757	99.3	154	2	Aaw04805	Human bet
14	757	99.3	154	2	Aaw06816	Human end
15	757	99.3	154	2	Aaw75414	Human bet
16	757	99.3	154	2	Aaw92283	Human bet
17	757	99.3	154	6	ABR63868	Thrombin
18	757	99.3	155	1	ADO55207	Sequence
19	757	99.3	155	1	AAP70482	Sequence
20	757	99.3	155	1	AAP94037	Human aci
21	757	99.3	155	2	AAR70812	FGF-1, 3/
22	757	99.3	155	2	AAR80776	Fibroblas
23	757	99.3	155	2	AAR75711	Fibroblas
24	757	99.3	155	2	AAR75415	Human end
25	757	99.3	155	2	Aaw53022	Fibroblas
					Aaw92291	Human end

26	757	99.3	155	2	AAV08588
27	757	99.3	155	3	AAV12333
28	757	99.3	155	3	AAV23233
29	757	99.3	155	3	AAV90410
30	757	99.3	155	3	AAV10297
31	757	99.3	155	4	AAV50705
32	757	99.3	155	4	AAV61661
33	757	99.3	155	4	AAV50298
34	757	99.3	155	4	AAV50273
35	757	99.3	155	4	AAV585812
36	757	99.3	155	5	AAV76943
37	757	99.3	155	5	AAV19990
38	757	99.3	155	5	AAV19394
39	757	99.3	155	6	AAV91200
40	757	99.3	155	6	AAV54277
41	757	99.3	155	6	AAV95452
42	757	99.3	155	7	ADCC34576
43	757	99.3	155	7	ABR56165
44	757	99.3	155	7	ADP66125
45	757	99.3	155	8	ADH92000
46	757	99.3	155	8	ADQ55201

ALIGNMENTS

RESULT 1	
AAR10527	
ID / AAR10527	standard; protein; 141 AA.
XX	
XX	
AC	AAR10527;
XX	
XX	
DT	25-MAR-2003 (revised)
DT	15-APR-1991 (first entry)
DT	
XX	
XX	
DE	Human acidic fibroblast growth factor gene.
DE	
XX	
KW	aFGF; antibody; antigen; cancer; ss.
XX	
OS	Homo sapiens.

XX Anti-acid antibody, for cancer diagnosis, etc. - is obtd. by using
PT complex of partial peptide(s) of acid fibroblast growth factor and
PT protein as antigen.
XX
PS Disclosure; Fig 1; 19pp; Japanese.
XX
XX The was deduced from a gene used to produce recombinant aFGF. Peptides
CC derived from the protein, esp. from A-B can be used to as antigens to
CC produce anti-aFGF antibodies. The peptides must comprise 8-10 continuous
CC AAs from A or B (claims 5 and 6 resp.), 7-10 continuous AAs from C (claim
CC 7).

7), or 8-9 continuous AAs from D (claim 8). The Abs can be used for immunochemically measuring aFGF, and for purifying aFGF. They are useful as reagents in the diagnosis of various cancers or diseases of the CNS. Purified aFGF has wound healing and nerve cell proliferating properties. (Updated on 25-MAR-2003 to correct PA field.)

CC Sequence 141 AA;
Query Match 100.0%; Score 762; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGDRSDQHIQLQLSAESVGEVYIKST 60
Db 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGDRSDQHIQLQLSAESVGEVYIKST 60
Qy 61 ETGOYLANDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Db 61 ETGOYLANDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 2
AAU76945
ID AAU76945 standard; protein; 141 AA.
XX AAU76945;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human acidic FGF protein HAEGF140.
XX
KW HAEGF140; acidic fibroblast growth factor; cell proliferation;
KW differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
KW human.
OS Homo sapiens.
OS Synthetic.
XX
FN WO200214471-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025537.
XX
PR 15-AUG-2000; 2000US-0225406P.
XX
PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX
PI Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
XX
DR WPI; 2002-257598/30.
DR N-PSDB; ABK10595.
XX
PT Producing a biologically active human acidic fibroblast growth factor
PT (haFGF) protein for use in promoting angiogenesis, involves employing an
PT E. coli transformed with a plasmid having an haFGF gene operably linked
PT to a promoter.
XX
PS Example 3; Fig 8; 41pp; English.
XX
CC This invention relates to a novel method for producing a biologically
CC active human acidic fibroblast growth factor (haFGF) protein. Fibroblast
CC growth factors are potent regulators of cell proliferation,
CC differentiation and normal development and they have been shown to play a
CC role in tumorigenesis and metastasis. Acidic fibroblast growth factor
CC has been shown to be potent inducers of angiogenesis. The gene for acidic
CC fibroblast growth factor is located on human chromosome 5. The method of
CC the invention comprises employing a plasmid having at least one copy of
CC gene, which encodes a biologically active haFGF protein operably linked

to a promoter, to transform Escherichia coli. The method is useful for producing recombinant or biologically active haFGF protein, which is useful in promoting angiogenesis. The present sequence represents the human acidic fibroblast growth factor 140 protein (haFGF140) used in the method of the invention

CC Sequence 141 AA;
Query Match 100.0%; Score 762; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGDRSDQHIQLQLSAESVGEVYIKST 60
Db 1 MFNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGDRSDQHIQLQLSAESVGEVYIKST 60
Qy 61 ETGOYLANDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Db 61 ETGOYLANDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 3
AAO19992
ID AAO19992 standard; protein; 141 AA.
XX AAO19992;
XX
DT 24-MAY-2002 (first entry)
XX
DE Protein of chemically synthesised human A FGF (140AA).
XX
KW Human acidic fibroblast growth factor; phage T7 polymerase promoter;
KW lysis; phage dependent superproduction; A FGF.
XX
OS Homo sapiens.
XX
FN WO200214468-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025477.
XX
PR 15-AUG-2000; 2000US-0225437P.
XX
PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX
PI Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
XX
DR WPI; 2002-269184/31.
DR N-PSDB; AAK98920.
XX
PT Bacteriophage-dependent method for producing biologically active proteins
PT or peptides, involves employing an Escherichia coli transformed with a
PT plasmid containing the targeted gene(s) operably linked to a promoter.
XX
PS Example 3; Fig 8; 44pp; English.
XX
CC The invention relates to a method for enhancing the production of a
CC biologically active protein comprising infecting a strain of Escherichia
CC coli, which has been transformed with a plasmid having at least one copy
CC of an expressible gene, such as a human acidic fibroblast growth factor.
CC The expressible gene encodes a biologically active protein operably
CC linked to a phage T7 polymerase promoter, with a bacteriophage capable of
CC mediating delayed lysis. The method is useful for the phage dependent
CC superproduction of biologically active protein and peptides. The method
CC is particularly useful for enhancing the production of heterologous
CC proteins in bacterial host cells. This sequence represents the protein of
CC a chemically synthesised human acidic fibroblast growth factor - human A
CC FGF (140AA) of the invention

```
XX SQ Sequence 141 AA;
Query Match 100.0%; Score 762; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPNGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60
Db 1 MFNLPNGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60

Qy 61 ETGOYLAMDTGGLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Db 61 ETGOYLAMDTGGLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141

RESULT 4
AD055206
ID AD055206 standard; protein; 141 AA.
AC AD055206;
XX
DT 09-SEP-2004 (first entry)
DE Human acidic fibroblast growth factor (hAFGF) seqid 7.
XX
KW neangiogenesis stimulator; cardiant; vasotropic; revascularisation;
KW ischaemic region; fibroblast growth factor-1; FGF-1; neoangiogenesis;
KW acidic FGF; aFGF; bacteriophage lambda; coronary artery disease;
KW myocardial perfusion; revascularisation therapy; ischaemic myocardium;
KW human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004115769-A1.
XX
PD 17-JUN-2004.
XX
PF 27-AUG-2003; 2003US-00649480.
XX
PR 24-JUL-1998; 98US-0093962P.
PR 22-JUL-1999; 99US-00358780.
PR 15-AUG-2000; 2000US-0225406P.
PR 15-AUG-2001; 2001US-00929945.
XX
XX (STEG/) STEGMANN T J.
PA (KORD/) KORDYUM V A.
PA (SLAV/) SLAVCHENKO I Y.
PA (CHER/) CHERNYKH S I.
PA (VOZI/) VOZIANOV O F.
XX
XX Stegmann TJ, Kordyum VA, Slavchenko IY, Chernykh SI, Vozianov OF;
PI WPI; 2004-449397/42.
DR N-PSDB; AD055205.
XX
XX Revascularizing an ischemic region, for treating coronary artery disease,
PT comprises preparing and injecting a composition comprising a recombinant
PT human fibroblast growth factor-1 into the ischemic region to induce local
PT neangiogenesis.
XX
XX Claim 12; SEQ ID NO 7; 42pp; English.
XX
XX The invention describes revascularising an ischaemic region comprising
CC preparing a pharmaceutical composition comprising a recombinant
CC fibroblast growth factor-1 (FGF-1) and injecting an amount of the
CC pharmaceutical composition into the ischaemic region, the amount being
CC sufficient to induce local neoangiogenesis. The FGF-1 is prepared by
```

```
CC transforming an Escherichia coli host cell with a plasmid comprising an
CC expressible gene encoding a biologically active human acidic FGF protein,
CC operably linked to a promoter; infecting the transformed bacterial host
CC cell with a bacteriophage  $\lambda$ gr; which mediates delayed lysis; and
CC cultivating the E. coli host cell under a culture condition that induces
CC lytic growth of the cell without lysis until a desired level of
CC production of the protein is reached, where the protein is produced as a
CC soluble, biologically-active human acidic FGF protein. Also described is
CC a method of treating coronary artery disease in a patient, comprising
CC preparing a pharmaceutical composition comprising a recombinant FGF-1;
CC injecting an amount of the pharmaceutical composition into at least one
CC site in a heart wall, the amount being sufficient to improve myocardial
CC perfusion; and injecting a composition comprising a physiological glue to
CC a surface of the heart at the site(s) where the pharmaceutical
CC composition was injected. The methods are useful for treating coronary
CC heart disease by revascularisation therapy or for inducing local
CC neoangiogenesis in ischaemic myocardium. This is the amino acid sequence
CC of human acidic fibroblast growth factor (hAFGF), the DNA encoding which
CC has been modified by substitution of naturally occurring codons with
CC codons found in highly expressed E.coli proteins.
XX
```

SQ Sequence 141 AA;

```
Query Match 100.0%; Score 762; DB 8; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPNGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60
Db 1 MFNLPNGNYKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVIYKST 60

Qy 61 ETGOYLAMDTGGLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120
Db 61 ETGOYLAMDTGGLYGSQTPNEECFLERLEENHYNTYISKHAEKNWFVGLKNGSCKR 120

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
Db 121 GPRTHYGOKAILFLPLPVSSD 141
```

RESULT 5

```
AAR05789
ID AAR05789 standard; protein; 151 AA.
XX
XX AAR05789;
AC AAR05789;
XX
DT 22-AUG-1990 (first entry)
XX
DE Human aFGF encoded by synthetic gene.
XX
XX Acidic fibroblast growth factor; aFGF; thrombogenesis; atherosclerosis;
KW tumors.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Key
FT Misc-difference 146..147
FT /note= "sites corresp. to two stop codons of the DNA
FT sequence"
XX
XX GB2223496-A.
XX
XX 11-APR-1990.
PD
XX
XX 08-AUG-1988; 88GB-00018775.
PF
XX
XX 08-AUG-1988; 88GB-00018775.
PR
XX
XX (BRBI-) BRIT BIO-TECH LTD.
PA
XX
XX Davies JA, Johnson ID;
PI
XX
XX WPI; 1990-109882/15.
DR
```

DR N-PSDB; AAQ03873.

XX Gene encoding human acidic fibroblast growth factor - incorporates useful
 PT restriction sites at frequent intervals to facilitate cassette
 PT mutagenesis of specified regions.

XX Claim 2; Fig 3a; 12pp; English.

XX The synthetic aFGF gene incorporates useful restriction sites at frequent
 CC intervals to facilitate the cassette mutagenesis of selected regions.
 CC Also included are flanking sites to simplify the incorporation of the
 CC gene into any expression system. The aFGF mol. acts in a cascade effect
 CC to control endothelial cell activity either co-ordinately through
 CC synergistic effects or via independent routes. The regulation of
 CC endothelial cells is essential for the protection of arteries, veins and
 CC capillaries from the effect of thrombogenesis. Their stimulation and
 CC control by these factors is also thought to be important in the
 CC development of tumours and atherosclerosis

XX Sequence 151 AA;

Query Match 100.0%; Score 762; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.8e-78;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTVDGTRDRSDQHIQLQLSAESVGEVIKST 60
 Db 5 MFNLPPGNYKKPKLLYCSNGGHFLRLIPDGTVDGTRDRSDQHIQLQLSAESVGEVIKST 64

Qy 61 ETGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKHAEKNWVGLKKGSCKR 120
 Db 65 ETGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKHAEKNWVGLKKGSCKR 124

Qy 121 GPRTHYGOKAILFLPLPVSSD 141
 Db 125 GPRTHYGOKAILFLPLPVSSD 145

RESULT 6

AAp70995

ID AAP70995 standard; protein; 140 AA.

XX AAP70995;

XX 13-JUN-1991 (first entry)

XX Sequence of human proteinaceous factor (PFI) with mitogenic activity.

XX Cell growth promoter; mitogen; vascularisation; wound healing.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 140

FT /label= Asp-OH

XX **EP241136-A.**

XX 14-OCT-1987.

XX 06-MAR-1987; 87EP-00301969.

XX 07-MAR-1986; 86US-00838096.

XX (HARD) HARVARD COLLEGE.

XX Lobb RR, Harper JW, Strydom DJ;

XX WPI; 1987-285995/41.

XX Mitogenic polypeptide isolated from human brain tissue - useful for
 PT increasing vascular effect in e.g. wound healing, or generating
 PT endothelial cell linings for vascular prostheses, etc.

XX Claim 3; Page 1; 31pp; English.

XX The PF of the invention was obt'd. from human brain tissue. It has a mol.
 CC wt. of 15,200-16,500 (pref. 15,616-16,056) and has a high affinity for
 CC heparin. PFI and fragments are useful for promoting the growth of
 CC mesoderm-derived cells or neuroectoderm-derived cells and generating
 CC endothelial cell linings for vascular prostheses (all claimed).The
 CC polypeptides are useful for increasing vascularisation

XX Sequence 140 AA;

Query Match 99.3%; Score 757; DB 1; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6.1e-78;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLIPDGTVDGTRDRSDQHIQLQLSAESVGEVIKSTE 61
 Db 1 FNLPPGNYKKPKLLYCSNGGHFLRLIPDGTVDGTRDRSDQHIQLQLSAESVGEVIKSTE 60

Qy 62 TGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKHAEKNWVGLKKGSCKR 121
 Db 61 TGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKHAEKNWVGLKKGSCKR 120

Qy 122 PRTHYGOKAILFLPLPVSSD 141
 Db 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 7

AAp90068

ID AAP90068 standard; protein; 140 AA.

XX AAP90068;

XX 25-MAR-2003 (revised)

DT 01-NOV-1989 (first entry)

XX Human acid fibroblast growth factor.

XX Human acidic fibroblast growth factor; mutant.

XX Homo sapiens.

XX **EP319052-A.**

XX 07-JUN-1989.

XX 14-OCT-1988; 88EP-00202306.

XX 22-OCT-1987; 87US-00112600.

XX 16-SEP-1988; 88US-00244431.

XX (MERI) MERCK & CO INC.

XX Thomas KA, Linemeyer DL;

XX WPI; 1989-167092/23.

XX Mutant acidic fibroblast growth factor - used for promoting repair of
 PT soft tissue, musculo-skeletal tissue or vascular or nerve tissue and
 PT plasminogen activator prodn.

XX Disclosure; Page 4; 36pp; English.

XX Amino acid sequence of human acidic fibroblast growth factor (aFGF). The
 CC patent claims mutant forms which have increased biological activity
 CC with(out) heparin, and promote cell growth. (Updated on 25-MAR-2003 to
 CC correct PD field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.)

XX Sequence 140 AA;

Query Match 99.3%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 121
DB 61 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 8
AAR25914
ID AAR25914 standard; peptide; 140 AA.
AC AAR25914;
XX
XX 25-MAR-2003 (revised)
DT 26-JAN-1993 (first entry)
XX
XX Human acidic fibroblast growth factor.
XX
XX viral infections; viruses; FGF; herpes simplex virus; HSV-1; HSV-2;
KW herpes varicella; herpes zoster; cytomegalovirus; influenza;
KW human respiratory syncytial virus; Semliki Forest virus; HIV;
KW human immunodeficiency virus; Moloney Sarcoma virus.
XX
OS Homo sapiens.
XX
XX EP497341-A2-
XX
XX 05-AUG-1992.
XX
XX 30-JAN-1992; 92EP-00101541.
XX
XX 31-JAN-1991; 91GB-00002145.
XX 09-JAN-1992; 92GB-00000410.
XX
XX (FARM) FARMITALIA ERBA SRL CARLO.
XX
XX Ungheri D, Garofano L, Battistini C, Carminati P, Mazue G;
XX
XX WPI; 1992-260792/32.
XX
XX Synergistic antiviral composition contains BFGF and sulphated
PT polysaccharide - for treating viral infections e.g. HSV-1 and -2,
PT cytomegalovirus, HIV, influenza virus etc.
XX
XX Disclosure; Page 4; 20pp; English.
XX
XX This sequence represents acidic fibroblast growth factor (aFGF). aFGF, or
CC its fragments may be used in a synergistic compen. with an antivirally
CC active sulphated polysaccharide, and one or more excipients. The compen.
CC may be used to control herpes simplex virus (HSV-1 or -2) herpes
CC varicella/zoster; cytomegalovirus; influenza; human respiratory syncytial
CC virus; Semliki Forest virus; HIV or Moloney Sarcoma virus. The
CC combination of aFGF with sulphated polysaccharide is found to have a
CC greater antiviral activity than expected for an additive effect. See also
CC AAR25913-5. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 140 AA;

Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 121
DB 61 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 9
AAR34497
ID AAR34497 standard; protein; 140 AA.
AC AAR34497;
XX
XX 06-AUG-1993 (first entry)
DT
XX Human acidic Fibroblast Growth Factor.
DE
XX aFGF; mutein; glycosylation site; glycoprotein.
KW
XX Homo sapiens.
OS
XX JP05076356-A.
XX
XX 30-MAR-1993.
PD
XX 30-MAY-1991; 91JP-00127435.
PF
XX 31-MAY-1990; 90JP-00143388.
PR
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-139564/17.
DR
XX
XX FGF mutein prep. useful for therapy of burn or thrombosis - by
PT transformation of lymphocyte-contained animal cell by vector contg. DNA
PT encoding FGF mutein.
XX
XX Disclosure; Page 3; 23pp; Japanese.
XX
XX The invention covers muteins of FGF (esp. bFGF) which contain at least
CC one glycosylation site. The muteins can be used to treat burns and
CC thrombosis
XX
XX Sequence 140 AA;

Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

QY 62 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 121
DB 61 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKNGSCCKRG 120

QY 122 PRTHYGOKAILFLPLPVSSD 141
DB 121 PRTHYGOKAILFLPLPVSSD 140

RESULT 10
AAR74647
ID AAR74647 standard; protein; 140 AA.
XX
XX AAR74647;
XX

DT 25-MAR-2003 (revised)
DT 25-SEP-1995 (first entry)
DE Human recombinant aFGF.
KW Acidic fibroblast growth factor; aFGF; vulnery; angiogenesis; mitogen.
XX Homo sapiens.
OS US5401832-A.
XX 28-MAR-1995.
PD
XX 25-SEP-1992; 92US-00951365.
PF 24-DEC-1984; 84US-00685923.
PR 12-SEP-1985; 85US-00774359.
PR 30-MAY-1986; 86US-00868473.
PR 11-JUL-1986; 86US-00884460.
PR 04-JUN-1987; 87US-00054991.
PR 04-MAY-1988; 88US-00190293.
PR 08-FEB-1991; 91US-00654397.
PR 25-SEP-1991; 91US-00765472.
XX (MERI) MERCK & CO INC.
FA Linemeyer DL, Thomas KA, Kelly LJ, Gimenez-Gallego G;
XX WPI; 1995-138983/18.
XX New recombinant human acidic fibroblast growth factor - used to promote
PT cell growth, to promote wound healing, for vascular grafts and blood
PT vessel repair.
XX Claim 2; Col 30; 25pp; English.
XX Oligonucleotides were synthesized on the basis of the amino acid sequence
CC of bovine acidic fibroblast growth factor (aFGF) and used to produce a
CC synthetic gene (given in AAQ88233) incorporating codons preferred by E.
CC coli or mammalian cells, unique cloning sites, etc. This synthetic gene
CC was mutagenized to obtain a gene encoding a human recombinant aFGF
CC (AAK74647) having activity equivalent to the native protein. (Updated on
CC 25-MAR-2003 to correct PF field.)
XX SQ Sequence 140 AA;
Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 60
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 121
DB 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 120
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 121 PRTHYGQKAILFLPLPVSSD 140
RESULT 11
AAW04806
ID AAW04806 standard; protein; 140 AA.
XX AC AAW04806;
XX 25-MAR-2003 (revised)
DT 29-DEC-1996 (first entry)
XX Human acidic fibroblast growth factor.

XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;
KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
XX fibroblast growth factor; ss.
OS Homo sapiens.
XX US552528-A.
XX 03-SEP-1996.
PD
XX 03-NOV-1994; 94US-00334884.
PF 03-MAR-1986; 86US-00835594.
PR 18-DEC-1987; 87US-00134499.
PR 29-APR-1991; 91US-00693079.
PR 27-NOV-1991; 91US-00799859.
XX (RHON) RHONE POULENC RORER PHARM INC.
FA Maciag T, Burgess W;
XX WPI; 1996-412132/41.
XX N-PSDB; AAT37503.
DR Isolated, purified, biologically active bovine beta endothelial cell
XX growth factor - useful to regenerate or treat damaged blood vessels.
PT Disclosure; Fig 8; 28pp; English.
PS Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a
XX mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain
CC using heparin-Sepharose affinity chromatography. ECGF is useful for,
CC among other purposes, diagnostic applications and has potential in the
CC treatment of damaged blood vessels or other endothelial cell-lined
CC structures. Human ECGF (AAT37503) or fragments may be obtained using
CC oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is
CC based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX SQ Sequence 140 AA;
Query Match 99.3%; Score 757; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.1e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 60
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 121
DB 61 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHYNTYISKHAEKNWVGLKKGCKRG 120
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 121 PRTHYGQKAILFLPLPVSSD 140
RESULT 12
AAW04805
ID AAW04805 standard; protein; 154 AA.
XX AC AAW04805;
XX 25-MAR-2003 (revised)
DT 29-DEC-1996 (first entry)
XX Human beta-endothelial cell growth factor.
XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;
KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
KW fibroblast growth factor.

```

XX Homo sapiens.
XX OS
XX PN US552528-A.
XX PD
XX PP 03-SEP-1996.
XX PF 03-NOV-1994; 94US-00334884.
XX PR 03-MAR-1986; 86US-00835594.
XX PR 18-DEC-1987; 87US-00134499.
XX PR 29-APR-1991; 91US-00693079.
XX PR 27-NOV-1991; 91US-00799859.
XX PA (RHON ) RHONE POULENC RORER PHARM INC.
XX PI Maciag T, Burgess W;
XX DR N-PSDB; AAT37503.
XX PT Isolated, purified, biologically active bovine beta endothelial cell
XX PT growth factor - useful to regenerate or treat damaged blood vessels.
XX PS Disclosure; Fig 8; 28pp; English.
XX CC Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a
XX CC mol. wt. of 20 kD can be purified at least 16300 fold from bovine brain
XX CC using heparin-Sepharose affinity chromatography. ECGF is useful for,
XX CC among other purposes, diagnostic applications and has potential in the
XX CC treatment of damaged blood vessels or other endothelial cell-lined
XX CC structures. Human ECGF (AAT37503) or fragments may be obtained using
XX CC oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is
XX CC based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-
XX CC 2003 to correct PF field.)
XX SQ Sequence 154 AA;

Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 61
DB 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 74
QY 62 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKKGSCRRG 121
DB 75 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKKGSCRRG 134
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 135 PRTHYGQKAILFLPLPVSSD 154

RESULT 13
AAW06816
ID AAW06816 standard; protein; 154 AA.
XX AC AAW06816;
XX XX
XX 25-MAR-2003 (revised)
XX DT 17-MAR-1997 (first entry)
XX XX
XX Human endothelial cell growth factor-beta.
XX DE Endothelial cell growth factor-beta; ECGF-beta.
XX KW Homo sapiens.
XX OS
XX PN US571790-A.
XX XX
XX 05-NOV-1996.
XX PD

Query Match 99.3%; Score 757; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 7e-78;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 61
DB 15 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHILQLLSAESVGEVYIKSTE 74
QY 62 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKKGSCRRG 121
DB 75 TGOYLAMDTGLLYGSQTPNEECFLERLEENHNTYISKHAEKNWVGLKKGSCRRG 134
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 135 PRTHYGQKAILFLPLPVSSD 154

RESULT 14
AAW75414
ID AAW75414 standard; protein; 154 AA.
XX AC AAW75414;
XX XX
XX 02-MAR-1999 (first entry)
XX DT
XX DE Human beta-endothelial cell growth factor.
XX XX
XX Human; endothelial cell growth factor; ECGF; brain stem; probe;
XX KW hybridisation; bovine; wound healing; prosthetic device.
XX XX
XX Homo sapiens.
XX OS
XX PN US5827826-A.
XX XX
XX 27-OCT-1998.
XX PD
XX PF 04-NOV-1996; 96US-00743261.
XX XX
XX 03-MAR-1986; 86US-00835594.
XX PR

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:42 ; Search time 28.5811 Seconds
(without alignments)
368.269 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPNGYKPKLLYCSNG.....PRTHYGOKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	762	100.0	141	4	US-09-929-945-7
2	762	100.0	141	4	US-09-929-918-7
3	757	99.3	140	1	US-07-830-330-6
4	757	99.3	140	6	5464943-28
5	757	99.3	140	6	5464943-28
6	757	99.3	154	4	US-09-929-945-8
7	757	99.3	155	1	US-08-439-725A-9
8	757	99.3	155	1	US-08-464-590A-13
9	757	99.3	155	1	US-08-462-169B-9
10	757	99.3	155	2	US-08-207-412B-8
11	757	99.3	155	2	US-08-867-471-9
12	757	99.3	155	2	US-08-951-822-29
13	757	99.3	155	3	US-09-103-079-9
14	757	99.3	155	3	US-08-705-245-5
15	757	99.3	155	3	US-08-718-904-10
16	757	99.3	155	3	US-09-023-082A-16
17	757	99.3	155	3	US-09-093-585-13
18	757	99.3	155	3	US-09-098-628-4
19	757	99.3	155	3	US-09-368-951-29
20	757	99.3	155	4	US-09-425-021-9
21	757	99.3	155	4	US-09-449-249-10
22	757	99.3	155	4	US-09-390-207-14
23	757	99.3	155	4	US-09-229-947-29
24	757	99.3	155	4	US-09-564-829-3
25	757	99.3	155	4	US-09-248-998-16
26	757	99.3	155	4	US-09-572-406B-7
27	757	99.3	155	4	US-09-490-714-5

28	757	99.3	155	4	US-09-929-945-2	Sequence 2, Appli
29	757	99.3	155	4	US-09-610-651-16	Sequence 16, Appli
30	757	99.3	155	4	US-09-929-918-2	Sequence 2, Appli
31	757	99.3	155	4	US-09-929-918-11	Sequence 11, Appli
32	755	99.1	155	2	US-08-438-439C-13	Sequence 13, Appli
33	746.5	98.0	156	3	US-09-030-613-15	Sequence 15, Appli
34	746.5	98.0	156	3	US-09-451-905-15	Sequence 15, Appli
35	734.5	96.4	191	2	US-08-438-439C-22	Sequence 22, Appli
36	732	96.1	140	4	US-09-417-721-1	Sequence 1, Appli
37	732	96.1	140	4	US-09-377-675A-8	Sequence 8, Appli
38	730	95.8	155	4	US-09-390-207-24	Sequence 24, Appli
39	727	95.4	136	6	5437995-2	Patent No. 5437995
40	727	95.4	136	6	5437995-2	Patent No. 5437995
41	721	94.6	135	4	US-09-929-945-5	Sequence 5, Appli
42	721	94.6	135	4	US-09-929-918-5	Sequence 5, Appli
43	697	91.5	140	1	US-07-830-330-7	Sequence 7, Appli
44	697	91.5	140	1	US-08-187-780-4	Sequence 4, Appli
45	697	91.5	140	2	US-08-478-485-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-929-945-7
; Sequence 7, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vorizanov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-945-7

Query Match	100.0%	Score	762;	DB	4;	Length	141;
Best Local Similarity	100.0%	Pred. No.	1.3e-80;				
Matches	141;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MFNLPNGYKPKLLYCSNGHFLRLPDGTGVDGTRDRSDQHIQLQLSAESVGEVYIKST	60				
Qy	61	ETGOVLAMDTGLLYGSOTPNEECFLERLENHNTYISKKHAEKNMFGVLKNGSCCKR	120				
Db	61	ETGOVLAMDTGLLYGSOTPNEECFLERLENHNTYISKKHAEKNMFGVLKNGSCCKR	120				
Qy	121	GPRTHYGOKAILFLPLPVSSD	141				
Db	121	GPRTHYGOKAILFLPLPVSSD	141				

RESULT 2

US-09-929-918-7
; Sequence 7, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vorizanov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Translated protein sequence for the chemically
; OTHER INFORMATION: synthesized 140 amino acid form of fibroblast
; OTHER INFORMATION: growth factor
US-09-929-918-7

Query Match 100.0%; Score 762; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKST 60
Db 1 MFNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKST 60

Qy 61 ETGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKR 120
Db 61 ETGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKR 120

Qy 121 GPRTHYGKAILFLPLPVSSD 141
Db 121 GPRTHYGKAILFLPLPVSSD 141

RESULT 3
US-07-830-330-6
; Sequence 6, Application US/07830330
; Patent No. 5288704
; GENERAL INFORMATION:
; APPLICANT: Ungheri, Domenico
; APPLICANT: Garofano, Luisa
; APPLICANT: Battistini, Carlo
; APPLICANT: Carminati, Paolo
; APPLICANT: Mazue, Guy
; TITLE OF INVENTION: SYNERGISTIC COMPOSITION COMPRISING A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND A SULFATED POLYSACCHARIDE,
; TITLE OF INVENTION: FOR USE AS ANTIVIRAL AGENT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ORLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C. C
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/830,330
; FILING DATE: 19920420
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5288704man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-230-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-07-830-330-6

Query Match 99.3%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 1 FNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

Qy 62 TGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKRG 121
Db 61 TGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKRG 120

Qy 122 PRTHYGKAILFLPLPVSSD 141
Db 121 PRTHYGKAILFLPLPVSSD 140

RESULT 4
5464943-28
; Patent No. 5464943
; APPLICANT: SENOO, MASAHARU; SASADA, REIKO; IGARASHI, KOICHI
; TITLE OF INVENTION: DNA ENCODING GLYCOSYLATED FGF AND
; PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,635
; FILING DATE: 15-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7,089
; FILING DATE: 19-JAN-1993
; APPLICATION NUMBER: 511,469
; FILING DATE: 20-APR-1990
; SEQ ID NO:28;
; LENGTH: 140
5464943-28

Query Match 99.3%; Score 757; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 1 FNLPNGYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

Qy 62 TGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKRG 121
Db 61 TGOYLAMDTDGLLYGSGTNPNEECFLERLEENHYNTYISKHAEKNWVGLKKGSCCKRG 120

Qy 122 PRTHYGKAILFLPLPVSSD 141
Db 121 PRTHYGKAILFLPLPVSSD 140

RESULT 5
5464943-28
; Patent No. 5464943
; APPLICANT: SENOO, MASAHARU; SASADA, REIKO; IGARASHI, KOICHI
; TITLE OF INVENTION: DNA ENCODING GLYCOSYLATED FGF AND
; PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,635
; FILING DATE: 15-JUL-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7,089
; FILING DATE: 19-JAN-1993
; APPLICATION NUMBER: 511,469
; FILING DATE: 20-APR-1990
; SEQ ID NO: 28
; LENGTH: 140
5464943-28

Query Match      99.3%; Score 757; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 1 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 60

QY 62 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 121
DB 61 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 120

QY 122 PRTHYGQKAILPLPVSSD 141
DB 121 PRTHYGQKAILPLPVSSD 140

RESULT 6
US-09-929-945-8
; Sequence 8, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-945-8

Query Match      99.3%; Score 757; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 15 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 74

QY 62 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 121
DB 75 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 134

QY 122 PRTHYGQKAILPLPVSSD 141
DB 135 PRTHYGQKAILPLPVSSD 154

RESULT 7
US-08-439-725A-9
; Sequence 9, Application US/08439725A
; Patent No. 5693775
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
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; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,725A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-439-725A-9

Query Match      99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

QY 62 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 121
DB 76 TCQYLAMDTDGLLYGSGTNPNEECLFLERLEENHNYTISKHAEKNWFGVGLKNGSKCRG 135

QY 122 PRTHYGQKAILPLPVSSD 141
DB 136 PRTHYGQKAILPLPVSSD 155

RESULT 8
US-08-464-590A-13
; Sequence 13, Application US/08464590A
; Patent No. 5763214
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESS: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,590A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-590A-13

Query Match          99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db      16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy      62 TGQYLDMTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 121
Db      76 TGQYLDMTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 135

Qy      122 PRTHYGQKAILFLPLPVSSD 141
Db      136 PRTHYGQKAILFLPLPVSSD 155

RESULT 9
US-08-462-169B-9
; Sequence 9, Application US/08462169B
; Patent No. 5773252
; GENERAL INFORMATION:
; APPLICANT: John Greene and Craig A. Rosen
; TITLE OF INVENTION: Fibroblast Growth Factor-15
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 05 JUN 95
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 155 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-462-169B-9

Query Match          99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db      16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

Qy      62 TGQYLDMTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 121
Db      76 TGQYLDMTDGLLYGSQTPNEECFLERLEENHYNTYISKHAENKWFVGLKKGSKCRG 135

Qy      122 PRTHYGQKAILFLPLPVSSD 141
Db      136 PRTHYGQKAILFLPLPVSSD 155

RESULT 10
US-08-207-412B-8
; Sequence 8, Application US/08207412B
; Patent No. 5817485
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; TITLE OF INVENTION: Fibroblast Growth Factor-10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,412B
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-412B-8

Query Match          99.3%; Score 757; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db      16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
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RESULT 12

Qy 122 PRTHYGQKAILFLPLPVSSD 141
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Db 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 14

US-08-705-245-5
; Sequence 5, Application US/08705245
; Patent No. 6020189
; GENERAL INFORMATION:
; APPLICANT: Nathans et al., Jeremy
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTORS (FhFs) AND METHODS OF USE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,245
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/094001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-50999
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-705-245-5

Query Match 99.3%; Score 757; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
|
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
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Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHNTYISKHAENWVGLKKGSCCKRG 121
|
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHNTYISKHAENWVGLKKGSCCKRG 135
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Qy 122 PRTHYGQKAILFLPLPVSSD 141
|
Db 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 15

US-08-718-904-10
; Sequence 10, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= "FGF-1"
; US-08-718-904-10

Query Match 99.3%; Score 757; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
|
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
|
Qy 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHNTYISKHAENWVGLKKGSCCKRG 121
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Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEENHNTYISKHAENWVGLKKGSCCKRG 135
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Qy 122 PRTHYGQKAILFLPLPVSSD 141
|
Db 136 PRTHYGQKAILFLPLPVSSD 155

Search completed: June 6, 2005, 07:47:28
Job time : 28.5811 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:37 ; Search time 22.8649 Seconds

(without alignments)
593.337 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPPGNYKKPKLLYCSNG.....PRTHYGQKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	757	99.3	155	1 A33665	acidic fibroblast
2	744	97.6	155	1 A60721	acidic fibroblast
3	730	95.8	155	2 D37360	acidic fibroblast
4	730	95.8	155	2 S04147	acidic fibroblast
5	727	95.4	152	2 JH0476	acidic fibroblast
6	697	91.5	155	1 GK80A	acidic fibroblast
7	689	90.4	155	2 JH0055	acidic fibroblast
8	678	89.0	155	2 A60130	acidic fibroblast
9	395	51.8	146	1 S00185	basic fibroblast g
10	395	51.8	157	1 GK80B	basic fibroblast g
11	394	51.7	189	2 A48834	basic fibroblast g
12	389	51.0	154	2 C37360	basic fibroblast g
13	389	51.0	154	2 A31674	basic fibroblast g
14	386	50.7	210	2 A32398	basic fibroblast g
15	380	49.9	164	2 S31622	basic fibroblast g
16	364	47.8	155	1 A40117	basic fibroblast g
17	361	47.4	137	2 I46711	fibroblast growth
18	251	32.9	211	2 JC7353	fibroblast growth
19	250	32.8	212	2 JC7511	fibroblast growth
20	249.5	32.7	208	2 S66486	fibroblast growth
21	249.5	32.7	208	2 A48137	fibroblast growth
22	247.5	32.5	208	2 JC7082	fibroblast somat
23	244.5	32.1	207	2 JC5941	fibroblast growth
24	240.5	31.6	207	2 JC5940	fibroblast growth
25	237.5	31.2	256	2 JH0708	fibroblast growth
26	232	30.4	60	2 JH0708	fibroblast growth
27	231.5	30.4	220	2 I50588	fibroblast growth
28	228.5	30.0	237	1 S39582	transforming prote
29	219	28.7	245	1 TVN5T2	

30	214	28.1	239	1 S04742	fibroblast growth
31	211	27.7	187	2 S23595	embryonic fibrobla
32	208.5	27.4	194	2 S49501	keratinocyte growt
33	206.5	27.1	194	2 I48610	keratinocyte growt
34	204.5	26.8	194	1 A36301	fibroblast growth
35	204.5	26.8	194	2 S26049	fibroblast growth
36	201.5	26.4	168	2 JG0184	fibroblast growth
37	201	26.4	192	2 S54407	embryonic fibrobla
38	200	26.2	264	2 A36207	fibroblast growth
39	200	26.2	266	2 S68144	fibroblast growth
40	198	26.0	194	2 I50710	fibroblast growth
41	197.5	25.9	413	2 H88481	protein let-756 (1
42	195	25.6	267	1 TVHUF5	fibroblast growth
43	191.5	25.1	125	2 A32484	basic fibroblast g
44	188	24.7	206	2 JC4268	fibroblast growth
45	185	24.3	206	1 TVHUMS	fibroblast growth

ALIGNMENTS

RESULT 1

A33665

acidic fibroblast growth factor 1 precursor [validated] - human

N:Alternate names: beta-ECGF; endothelial cell growth factor beta; heparin-binding growth

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C:Accession: A33665; A32316; S18217; A43804; A24662; JH0707; S35535; S35536; I39413; A23:

R:Merz, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abrah

Biochem. Biophys. Res. Commun. 164, 1121-1129, 1989

A:Title: Structural analysis of the gene for human acidic fibroblast growth factor.

A:Reference number: A33665; MUID:90073637; PMID:2590193

A:Accession: A33665

A:Molecule type: DNA

A:Residues: 1-155 <MER>

A:Cross-references: UNIPROT:P05230; GB:M30491

R:Wang, W.P.; Lehtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.

Mol. Cell. Biol. 9, 2387-2395, 1989

A:Title: Cloning of the gene coding for human class 1 heparin-binding growth factor and

A:Reference number: A32316; MUID:89343957; PMID:2474753

A:Accession: A32316

A:Molecule type: DNA

A:Residues: 1-155 <WAN>

A:Cross-references: GB:M23087; NID:G183875; PIDN:AAA52638.1; PID:G386768

R:Wang, W.P.; Quick, D.; Balcerzak, S.P.; Needleman, S.W.; Chiu, I.M.

Oncogene 6, 1521-1529, 1991

A:Title: Cloning and sequence analysis of the human acidic fibroblast growth factor gene

A:Reference number: S18217; MUID:92019819; PMID:1717925

A:Accession: S18217

A:Molecule type: DNA

A:Residues: 1-155 <WAZ>

A:Cross-references: EMBL:M23086

R:Chiu, I.M.; Wang, W.P.; Lehtoma, K.

Oncogene 5, 755-762, 1990

A:Title: Alternative splicing generates two forms of mRNA coding for human heparin-bindin

A:Reference number: A43804; MUID:90265618; PMID:1693186

A:Accession: A43804

A:Molecule type: mRNA

A:Residues: 1-155 <CHI>

A:Cross-references: EMBL:X51943; NID:G32435; PIDN:CAA36206.1; PID:G32436

R:Jaye, M.; Hawk, R.; Burgess, W.; Ricca, G.A.; Chiu, I.M.; Ravera, M.M.; O'Brien, S.J.;

Science 233, 541-545, 1986

A:Title: Human endothelial cell growth factor: cloning, nucleotide sequence, and chromos

A:Reference number: A24662; MUID:86261805; PMID:3523756

A:Accession: A24662

A:Molecule type: mRNA

A:Residues: 1-155 <JAY>

A:Cross-references: GB:M13361; NID:G181941; PIDN:AAA79245.1; PID:G181942

R:Yu, Y.L.; Kha, H.; Golden, J.A.; Migchelsen, A.A.J.; Goatzl, E.J.; Turck, C.W.

J. Exp. Med. 175, 1073-1080, 1992

A:Title: An acidic fibroblast growth factor protein generated by alternate splicing act

A:Reference number: JH0707; MUID:92202857; PMID:1372643

A:Accession: JH0707

A;Molecule type: mRNA
A;Residues: 1-155 <YU>
A;Cross-references: GB:X65778; NID:G396163; PIDN:CAA46661.1; PID:G396164
R;Payson, R.A.; Canatani, H.; Chotani, M.A.; Wang, W.P.; Harris, S.E.; Myers, R.L.; Chiu, Nucleic Acids Res. 21, 489-495, 1993
A;Title: Cloning of two novel forms of human acidic fibroblast growth factor (aFGF) mRNA
A;Reference number: S35535; MUID:93181239; PMID:7680120
A;Accession: S35535
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-58 <PAY>
A;Cross-references: GB:L01485
A;Accession: S35536
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-58 <PA2>
A;Cross-references: GB:L01487
R;Crumley, G.; Dionne, C.A.; Jaye, M., Biochem. Biophys. Res. Commun. 171, 7-13, 1990
A;Title: The gene for human acidic fibroblast growth factor encodes two upstream exons and a 3' noncoding region
A;Reference number: I39412; MUID:90365758; PMID:2393407
A;Accession: I39413
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 <RES>
A;Cross-references: GB:M60515; NID:G178226; PIDN:AAA51672.1; PID:G553170; GB:M60516; NID:G178226
R;Harper, J.W.; Strydom, D.J.; Lobb, R.R. Biochemistry 25, 4097-4103, 1986
A;Reference number: A23553; MUID:86296647; PMID:2427112
A;Accession: A23553
A;Molecule type: protein
A;Residues: 16-155 <HAR>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A. Biochem. Biophys. Res. Commun. 138, 611-617, 1986
A;Title: The complete amino acid sequence of human brain-derived acidic fibroblast growth factor
A;Reference number: A24820; MUID:86295741; PMID:3527167
A;Accession: A24820
A;Molecule type: protein
A;Residues: 16-155 <GIM>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A. Biochem. Biophys. Res. Commun. 135, 541-548, 1986
A;Title: Human brain-derived acidic and basic fibroblast growth factors: amino terminal regions are identical
A;Reference number: A90122; MUID:86186784; PMID:3964259
A;Accession: A24243
A;Molecule type: protein
A;Residues: 16-47 <GI2>
R;Experimental source: brain
R;Gautschi, P.; Frater-Schroder, M.; Bohlen, P. FEBS Lett. 204, 203-207, 1986
A;Title: Partial molecular characterization of endothelial cell mitogens from human brain
A;Reference number: A91364; MUID:86275260; PMID:3732516
A;Accession: A24301
A;Molecule type: protein
A;Residues: 16-30, 'X', 32-49 <GAU>
R;Gautschi-Sova, P.; Muller, T.; Bohlen, P. Biochem. Biophys. Res. Commun. 140, 874-880, 1986
A;Title: Amino acid sequence of human acidic fibroblast growth factor.
A;Reference number: A26386; MUID:87048871; PMID:3778488
A;Accession: A26386
A;Molecule type: protein
A;Residues: 16-155 <GA2>
R;Experimental source: brain
R;Chavan, A.J.; Haley, B.E.; Volkin, D.B.; Marfia, K.E.; Verticelli, A.M.; Bruner, M.W.; Biochemistry 33, 7193-7202, 1994
A;Title: Interaction of nucleotides with acidic fibroblast growth factor (FGF-1).
A;Reference number: A53639; MUID:94271773; PMID:7516183
A;Accession: A53639
A;Molecule type: protein
A;Residues: 16-30, 'X', 32-38; 73-75, 'X', 77-97, 'X', 99-101; 128-131, 'X', 133-140, 'X', 142-152 <FGF1>
C;Genetics:
A;Gene: GDB:FGF1; FGFA
A;Cross-references: GDB:I19909; OMTM:131220
A;Map position: 5q31.3-5q33.2

A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
C;Keywords: alternative splicing; growth factor; heparin binding
F;16-155/Product: fibroblast growth factor 1 #status experimental <MAT>
F;129/Binding site: carbohydrate (Asn) (covalent) #status absent
Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 4.1e-65;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVVIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVVIKSTE 75
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEBNHYNTYISKKHAENKMFVGLKKGSKCRG 121
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEBNHYNTYISKKHAENKMFVGLKKGSKCRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
Db 136 PRTHYGQKAILFLPLPVSSD 155
RESULT 2
A60721
acidic fibroblast growth factor - golden hamster
N;Alternate names: heparin-binding growth factor 1
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A60721
R;Hall, J.A.; Harris, M.A.; Malark, M.; Manseon, P.E.; Zhou, H.; Harris, S.E. J. Cell. Biochem. 43, 17-26, 1990
A;Title: Characterization of the hamster DDT-1 cell aFGF/HGBF-I gene and its mRNA
A;Reference number: A60721; MUID:90270291; PMID:1693366
A;Accession: A60721
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-155 <HAL>
A;Cross-references: UNIPROT:P34004
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
Query Match 97.6%; Score 744; DB 1; Length 155;
Best Local Similarity 97.9%; Pred. No. 7.2e-64;
Matches 137; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVVIKSTE 61
Db 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVVIKSTE 75
QY 62 TGOYLAMDTDGLLYGSQTPNEECFLERLEBNHYNTYISKKHAENKMFVGLKKGSKCRG 121
Db 76 TGOYLAMDTDGLLYGSQTPNEECFLERLEBNHYNTYISKKHAENKMFVGLKKGSKCRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
Db 136 PRTHYGQKAILFLPLPVSSD 155
RESULT 3
D37360
acidic fibroblast growth factor - mouse
N;Alternate names: aFGF; FGF-1
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: D37360; JCS231
R;Hebert, J.M.; Basilio, C.; Goldfarb, M.; Haub, O.; Martin, G.R. Dev. Biol. 138, 454-463, 1990
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns
A;Reference number: A37360; MUID:90201563; PMID:2318343
A;Accession: D37360
A;Status: preliminary
A;Molecule type: mRNA

A:Residues: 1-155 <HEB>
A:Cross-references: UNIPROT:P61148; GB:M30641; NID:gl93284; PIDN:AAA37618.1; PID:G309236
R:Madhavi, P.; Hackshaw, K.V.; Chiu, I.M.
Gene 179, 231-236, 1996
A:Title: Cloning and characterization of the mouse Fgf-1 gene.
A:Reference number: JCS231; MUID:97128312; PMID:8972905
A:Accession: JCS231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <MAD>
A:Cross-references: GB:U36456
C:Comment: This protein is an inducer of neovascularization in angiogenic disease includ
C:Genetics:
A:Gene: Fgf-1
A:Introns: 57/1, 91/3
C:Superfamily: fibroblast growth factor

Query Match 95.8%; Score 730; DB 2; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.6e-62;
Matches 135; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPLGNKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 4
S04147
acidic fibroblast growth factor 1 - rat
N:Alternate names: heparin-binding growth factor 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04147
R:Goodrich, S.P.; Yan, G.C.; Bahrenburg, K.; Mansson, P.E.
Nucleic Acids Res. 17, 2867, 1989
A:Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A:Reference number: S04147; MUID:89240051; PMID:2470029
A:Accession: S04147
A:Molecule type: mRNA
A:Residues: 1-155 <GOO>
A:Cross-references: UNIPROT:P61149; EMBL:X14232; NID:G56351; PIDN:CAA32448.1; PID:G56352
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding

Query Match 95.8%; Score 730; DB 2; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.6e-62;
Matches 135; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPLGNKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 5
JH0476
acidic fibroblast growth factor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0476; S20072
R:Schmidt, M.; Sharma, H.S.; Schott, R.J.; Schaper, W.
Biochem. Biophys. Res. Commun. 180, 853-859, 1991
A:Title: Amplification and sequencing of mRNA encoding acidic fibroblast growth factor (a
A:Reference number: JH0476; MUID:92062117; PMID:1719973
A:Accession: JH0476
A:Molecule type: mRNA
A:Residues: 1-152 <SCH>
A:Cross-references: UNIPROT:P20002; EMBL:X60317; NID:G1873; PIDN:CAA42869.1; PID:G1874
A:Experimental source: heart
A:Note: The hydrophobic core residues are packed around the internal symmetry axis
C:Comment: This protein belongs to the fibroblast growth factor family.
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding
F:22-28/Region: nuclear location signal
F:133/Binding site: heparin (Lys) #status predicted

Query Match 95.4%; Score 727; DB 2; Length 152;
Best Local Similarity 97.8%; Pred. No. 3e-62;
Matches 134; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPGNYKKPKLLYCSNGGHLRLIPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75
QY 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 121
DB 76 TGOYLAMTEGLLYGSQTPNEECFLERLEENHNYTYSKKHAENKWFVGLKKNKSGCKRG 135
QY 122 PRTHYGQKAILFLPLPV 138
DB 136 PRTHYGQKAILFLPLPV 152

RESULT 6
GKBOA
acidic fibroblast growth factor precursor - bovine
N:Alternate names: aFGF; eye-derived growth factor II; heparin-binding growth factor I;
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Aug-1986 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: JH0613; S02102; S02661; S22065; B24663; A94281; S03953; A91010; A24477; B25
R:Renard, F.; Desset, S.; Bugra, K.; Halley, C.; Philippe, J.M.; Courtois, Y.; Laurent, M.
Biochem. Biophys. Res. Commun. 184, 945-952, 1992
A:Title: Heterogeneity of 3' untranslated region of bovine acidic FGF transcripts.
A:Reference number: JH0613; MUID:92246990; PMID:1374244
A:Accession: JH0613
A:Molecule type: DNA
A:Residues: 58-155 <REN>
A:Cross-references: UNIPROT:P03968
R:Halley, C.; Courtois, Y.; Laurent, M.
Nucleic Acids Res. 16, 10913, 1988
A:Title: Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.
A:Reference number: S02102; MUID:89083506; PMID:3205724
A:Accession: S02102
A:Molecule type: mRNA
A:Residues: 1-155 <HAL>
A:Cross-references: EMBL:X13221; NID:G347; PIDN:CAA31610.1; PID:G348
R:Alterio, J.; Halley, C.; Brou, C.; Soussi, T.; Courtois, Y.; Laurent, M.
FEBS Lett. 242, 41-46, 1988
A:Title: Characterization of a bovine acidic FGF cDNA clone and its expression in brain
A:Reference number: S02661; MUID:89078619; PMID:2849564
A:Accession: S02661
A:Molecule type: mRNA
A:Residues: 1-155 <ALT>
A:Cross-references: EMBL:X14032; NID:G322; PIDN:CAA32192.1; PID:G323
R:Philippe, J.M.
Submitted to the EMBL Data Library, May 1992
A:Reference number: S22065
A:Accession: S22065
A:Molecule type: mRNA
A:Residues: 1-18 <PHI>
A:Cross-references: EMBL:X66446; NID:G411; PIDN:CAA47063.1; PID:G412

R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gosp Science 233, 545-548, 1986
A;Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fi
A;Reference number: A94290; MUID:86261806; PMID:2425435
A;Accession: B24663
A;Molecule type: mRNA
A;Residues: 16-56 <ABR>
R;Gimenez-Gallego, G.; Rodkey, J.; Bennett, C.; Rios-Candelore, M.; DiSalvo, J.; Thomas, Science 230, 1385-1388, 1985
A;Title: Brain-derived acidic fibroblast growth factor: complete amino acid sequence and
A;Reference number: A94281; MUID:86070224; PMID:4071057
A;Accession: A94281
A;Molecule type: protein
A;Residues: 16-155 <GRM>
R;Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethke, N.; Sharma, H.S.; Schape Eur. J. Biochem. 181, 67-73, 1989
A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A;Reference number: S03953; MUID:89231704; PMID:2714282
A;Accession: S03953
A;Molecule type: protein
A;Residues: 16-45 <QUT>
R;Bohlen, P.; Esch, F.; Baird, A.; Gospodarowicz, D.
EMBO J. 4, 1951-1956, 1985
A;Title: Acidic fibroblast growth factor (FGF) from bovine brain: amino-terminal sequenc
A;Reference number: A91010; MUID:86055750; PMID:4065099
A;Accession: A91010
A;Molecule type: protein
A;Residues: 16-30,'X',32-34,'X',36-44 <BOH>
R;Crabb, J.W.; Ames, L.G.; Carr, S.A.; Johnson, C.M.; Roberts, G.D.; Bordoli, R.S.; McK Biochemistry 25, 4988-4993, 1986
A;Title: Complete primary structure of prostatin, a prostate epithelial cell growth f
A;Reference number: A24477; MUID:87026586; PMID:3768327
A;Accession: A24477
A;Molecule type: protein
A;Residues: 2,'GE',5-155 <CRA>
R;Burgess, W.H.; Mehlman, T.; Marshak, D.R.; Fraser, B.A.; Maciag, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 7216-7220, 1986
A;Title: Structural evidence that endothelial cell growth factor beta is the precursor c
A;Reference number: A94127; MUID:87016918; PMID:3532107
A;Accession: B25043
A;Molecule type: protein
A;Residues: 2-155 <BUR>
A;Note: this form was designated beta endothelial cell growth factor
A;Accession: C25043
A;Molecule type: protein
A;Residues: 16-155 <BU2>
A;Note: this form was designated acidic fibroblast growth factor
A;Accession: A25043
A;Molecule type: protein
A;Residues: 22-155 <BU3>
A;Note: this form was designated alpha endothelial cell growth factor
R;Strydom, D.J.; Harper, J.W.; Lobb, R.R.
Biochemistry 25, 945-951, 1986
A;Title: Amino acid sequence of bovine brain derived class 1 heparin-binding growth fact
A;Reference number: A24539; MUID:86187766; PMID:2421762
A;Accession: A24539
A;Molecule type: protein
A;Residues: 16-155 <STR>
R;Thomas, K.A.; Gimenez-Gallego, G.; Rios-Candelore, M.; DiSalvo, J.
J. Protein Chem. 6, 163-171, 1987
A;Title: Primary structure and mitogenic and angiogenic activities of brain-derived acid
A;Reference number: A60884
A;Accession: A60884
A;Molecule type: protein
A;Residues: 16-155 <THO>
R;Kuo, W.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 265, 16455-16463, 1990
A;Title: Acidic fibroblast growth factor receptor purified from bovine liver is a novel
A;Reference number: A37892; MUID:90375514; PMID:2168890
A;Accession: A37892
A;Molecule type: protein
A;Residues: 22-30,'X',32-38 <KU2>
A;Note: this form was designated brain-derived growth factor A

A;Accession: B37892
A;Molecule type: protein
A;Residues: 16-30,'X',32-40 <KUO>
A;Note: this sequence is an amino-terminal fragment of a form designated as brain-derived
R;Hill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
Brain Res. Dev. Brain Res. 63, 13-19, 1991
A;Title: Class 1 heparin binding growth factor promotes the differentiation but not the
A;Reference number: A61198; MUID:92164087; PMID:1724209
A;Accession: A61198
A;Molecule type: protein
A;Residues: 11-26;28-50;53-110,'H',112,'NTY';134-155 <HIL>
R;Philippe, J.M.; Renaud, F.; Desset, S.; Laurent, M.; Mallet, J.; Courtois, Y.; Edwards, Biochem. Biophys. Res. Commun. 188, 843-850, 1992
A;Title: Cloning of two different 5' untranslated exons of bovine acidic fibroblast growth
A;Reference number: I46024; MUID:93075172; PMID:1280126
A;Accession: I46024
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-18 <PH2>
A;Cross-references: EMBL:X66446; NID:G411; PIDN:CAA47063.1; PID:G412
R;Sasaki, H.; Hoshi, H.; Hong, Y.M.; Suzuki, T.; Kato, T.; Sasaki, H.; Saito, M.; Youki, J. Biol. Chem. 264, 17606-17612, 1989
A;Title: Purification of acidic fibroblast growth factor from bovine heart and its local
A;Reference number: A34477; MUID:90008933; PMID:2677012
A;Accession: A34477
A;Status: preliminary
A;Molecule type: protein
A;Residues: 16-24;121-127;134-143 <SAS>
A;Experimental source: heart
C;Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating t
f these two growth factors.
C;Comment: This protein binds heparin, although less strongly than does bFGF.
C;Comment: There are some sequence similarities between residues 117-126 (a region flank
sides 18-27) and bovine substance P beta (residues 98-107).
C;Genetics:
A;Gene: HBGF-1
A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
C;Keywords: acetylated amino end; angiogenesis; growth factor; heparin binding; mitogen
F;2-155/Product: beta endothelial cell growth factor #status experimental <ECB>
F;16-155/Product: acidic fibroblast growth factor #status experimental <MAT>
F;22-155/Product: alpha endothelial cell growth factor #status experimental <SCA>
F;24-28,113-116/Region: heparin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
Query Match 91.5%; Score 697; DB 1; Length 155;
Best Local Similarity 92.1%; Pred. No. 2.2e-59;
Matches 129; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 2 FNLPNGYKKPKLLYCSNGGHFLRLPDGTVDGTRDSQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPNGYKKPKLLYCSNGGYFRLPDGTVDGTRDSQHIQLQCAESIGEVIKSTE 75
Qy 62 TGOYLAAMDTPGLYGSQTPNEECFLERLENHYNTYISKHAEKWNFWGLKKNKSCKRG 121
Db 76 TGOFLAMDTDGLLYGSQTPNEECFLERLENHYNTYISKHAEKWNFWGLKKNKRSKLG 135
Qy 122 PRHYGQKAILFLPLPVSSD 141
Db 136 PRTHFGQKAILFLPLPVSSD 155
RESULT 7
JW0055
acidic fibroblast growth factor 1 precursor - sheep
N;Alternate names: FGF-1
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: JW0055
R;Grieb, T.W.; Ring, M.; Brown, E.; Palmer, C.; Belle, N.; Donjerkovic, D.; Chang, H.; Yi Biochem. Biophys. Res. Commun. 246, 182-191, 1998
A;Title: Primary structure of ovine fibroblast growth factor-1 deduced by protein and cd

A:Reference number: JW0055; MUID:98262939; PMID:9600090
A:Accession: JW0055
A:Molecule type: mRNA
A:Residues: 1-155 <GRI>
A:Cross-references: UNIPROT:Q7M303
C:Comment: This protein is a potent mitogenic factor for NIH 3T3 fibroblasts in the absence of growth factor
C:Superfamily: fibroblast growth factor

Query Match 90.4%; Score 689; DB 2; Length 155;
Best Local Similarity 90.7%; Pred. No. 1.3e-58;
Matches 127; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 2 FNLPGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESGEVYIKSTE 61
DB 16 FNLPGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESGEVYIKSTE 75
QY 62 TQOYLAMDTGLLYGSQTPNEBCLFLERLEENHYNTYISKHAEKNWVGLKNGSCXRG 121
DB 76 TQOYLAMDTGLLYGSQTPNEBCLFLERLEENHYNTYISKHAEKNWVGLKNGSCXRG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 8
Ae0130
acidic fibroblast growth factor - chicken
N:Alternate names: endothelial cell growth factor
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
A:Accession: Ae0130; S02639
R:Schneider, H.; Risau, W.
Development 111, 1143-1154, 1991
A:Title: Differentiating and mature neurons express the acidic fibroblast growth factor
A:Reference number: Ae0130; MUID:91347925; PMID:1715259
A:Accession: Ae0130
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <SCH>
A:Cross-references: UNIPROT:P19596; GB:S63263; NID:G234372; PIDN:AA819629.1; PID:G234373
R:Risau, W.; Gautschi-Sova, P.; Boehlen, P.
EMBO J. 7, 959-962, 1988
A:Title: Endothelial cell growth factors in embryonic and adult chick brain are related
A:Reference number: S02639; MUID:88296438; PMID:3402441
A:Accession: S02639
A:Molecule type: protein
A:Residues: 22-30,'X',32-44,'X',46-48 <RIS>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor

Query Match 89.0%; Score 678; DB 2; Length 155;
Best Local Similarity 90.0%; Pred. No. 1.5e-57;
Matches 126; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 2 FNLPGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESGEVYIKSTE 61
DB 16 FGLPLGNKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAEDVGEVYIKSTA 75
QY 62 TQOYLAMDTGLLYGSQTPNEBCLFLERLEENHYNTYISKHAEKNWVGLKNGSCXRG 121
DB 76 SQOYLAMDTGLLYGSQTPNEBCLFLERLEENHYNTYISKHAEKNWVGLKNGSKLG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 9
S00185
basic fibroblast growth factor - sheep
N:Alternate names: prostatripin
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S00185
R:Simpson, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, L.J.; Nice, E.C.; Rubira, M.R.; Burger
FEBS Lett. 224, 128-132, 1987
A:Title: Primary structure of ovine pituitary basic fibroblast growth factor.
A:Reference number: S00185; MUID:88055577; PMID:3678486
A:Accession: S00185
A:Molecule type: protein
A:Residues: 1-146 <SIM>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding; mitogen
F:18-22/Region: heparin binding #status predicted
F:107-110/Region: heparin binding #status predicted

Query Match 51.8%; Score 395; DB 1; Length 146;
Best Local Similarity 56.6%; Pred. No. 1.5e-30;
Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;
QY 5 PPGNYKKPKLLYCSNGGHFLRLPDGTVGDRDRSDQHIQLQLSAESGEVYIKSTETGQ 64
DB 13 PPGHFKDPRLYCKNGGFFLRHPDGRVDGVREKSDPHIKLQQAEEGVVSIKGVCANR 72
QY 65 YLAMDTGLLYGSQTPNEBCLFLERLEENHYNTYISKHAEKNWVGLKNGSCXRGPR 124
DB 73 YLAMKEDGRLLASKCVTDECFEERLESNNYNTYRSKYS--SWYVALKRTGQYKLGPKT 130
QY 125 HYGQKAILFLPLPVSS 140
DB 131 GFGQKAILFLPMSAKS 146

RESULT 10
GABOB
basic fibroblast growth factor precursor - bovine (fragment)
N:Alternate names: bFGF; kidney-derived growth factor; prostatripin
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Aug-1986 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
A:Accession: A24663; A32878; A33784; A61550; A61551; A61094; A01386; A60316; A221
R:Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gospo
Science 233, 545-548, 1986
A:Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fib
A:Reference number: A94290; MUID:86261806; PMID:2425435
A:Accession: A24663
A:Molecule type: mRNA
A:Residues: 3-157 <ABR>
A:Cross-references: UNIPROT:P03969; GB:M13440; NID:G163049; PIDN:AAA30518.1; PID:G163050
A:Experimental source: pituitary gland
R:Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Fiddes, J.C.
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
A:Title: Human basic fibroblast growth factor: nucleotide sequence, genomic organization,
A:Reference number: A90924; MUID:87217066; PMID:3472745
A:Accession: A32878
A:Molecule type: mRNA
R:Minner, P.G.; Li, Y.S.; Hoffman, R.M.; Kodner, C.M.; Siegel, N.R.; Deuel, T.F.
Biochem. Biophys. Res. Commun. 165, 1096-1103, 1989
A:Title: A novel 17 kD heparin-binding growth factor (HBGF-8) in bovine uterus: purifica
A:Reference number: A33784; MUID:90121211; PMID:2610682
A:Accession: A33784
A:Molecule type: protein
A:Residues: 1-14 <MIL>
A:Note: demonstration of a possible alternative initiator or splice junction
R:Botolini, J.; Hearn, M.T.W.
Mol. Cell. Endocrinol. 51, 187-199, 1987
A:Title: Isolation, characterization and tissue localisation of an N-terminal-truncated v
A:Reference number: A61550; MUID:87247652; PMID:3596000
A:Accession: A61550
A:Molecule type: protein
A:Residues: 16-35 <BER>
R:Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.
Mol. Cell. Endocrinol. 49, 189-194, 1987
A:Title: Isolation and partial characterization of basic fibroblast growth factor from b
A:Reference number: A61551; MUID:87162856; PMID:3556754


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Db      137 YLAKMEDGRLLASKCVTDCEFFERLESNNYNTYRSRKYT--SWYVALKRTQYKLGSKT 194
Qy      125 HYGQKAILFLPLPVSS 140
      |||||||:|
Db      195 GPGQKAILFLPMSAKS 210

RESULT 15
S31622
basic fibroblast growth factor - short-tailed opossum (Monodelphis domestica) (fragment)
C;Species: Monodelphis domestica
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C;Accession: S31622
R;Kusewitt, D.F.; Sabourin, C.L.K.; Budge, C.L.; Ley, R.D.
submitted to the EMBL Data Library, September 1992
A;Description: Characterization of cDNA encoding basic fibroblast growth factor of the m
A;Reference number: S31622
A;Accession: S31622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-164 <KUS>
A;Cross-references: EMBL:Z15154
C;Superfamily: fibroblast growth factor

Query Match      49.9%; Score 380; DB 2; Length 164;
Best Local Similarity 55.9%; Pred. No. 4.7e-29;
Matches 76; Conservative 16; Mismatches 42; Indels 2; Gaps 1;

Qy      5 PPGNYKKPLLYCSNGGHFLRILPDGTVDGTRDSQHTQLQLSAESVGEVYIKSTETGQ 64
      |||:| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      31 PPGHFDPKRLYCKNGGFLRIHPDGRVDGIREKSDPNIKLQLQAEERGWSIKGVCANR 90
      ||| ||| ||| :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      65 YLAMDTDGLLYGSGOTPNEECLFLERLEENHYNTYISKHAENKWFVGLKKGKSGCKRGPR 124
      ||| ||| ||| :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      91 YLAKMEDGRLLALKYVTEECFFERLESNNYNTYRSRKYS--NWYVALKRTQYKLGSKT 148
      ||| ||| ||| :| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      125 HYGQKAILFLPLPVSS 140
      |||||||:|
Db      149 GPGQKAILFLPMSAKS 164

Search completed: June 6, 2005, 07:46:22
Job time : 23.8649 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2005, 07:37:37 ; Search time 107.179 Seconds

(without alignments)

673.669 Million cell updates/sec

Title: US-10-649-480A-7

Perfect score: 762

Sequence: 1 MFNLPNGYKPKLLYCSNG.....PRTHYQKAILFLPLPVSSD 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	757	99.3	155	1 FGF1_HUMAN	P05230 homo sapien
2	744	97.6	155	1 FGF1_MESAU	P34004 mesocricetu
3	730	95.8	155	1 FGF1_MOUSE	P61148 mus musculus
4	730	95.8	155	1 FGF1_RAT	P61149 rattus norv
5	727	95.4	152	1 FGF1_PIG	P20002 sus scrofa
6	697	91.5	155	1 FGF1_BOVIN	P03968 bos taurus
7	689	90.4	155	1 FGF1_SHEEP	Q7m303 ovis aries
8	678	89.0	155	1 FGF1_CHICK	P19596 gallus gall
9	612	80.3	148	1 FGF1_CYNPY	Q616m7 cynops pyrr
10	579	76.0	155	1 FGF1_XENLA	Q6glr6 xenopus lae
11	571	74.9	132	1 FGF1_NOTVI	Q7sif8 notophthalm
12	529	69.4	106	1 FGF1_CAPCA	Q9n1s8 capreolus c
13	395	51.8	154	2 Q7ZZK5	P03968 bos taurus
14	395	51.8	155	1 FGF2_BOVIN	P03969 bos taurus
15	395	51.8	155	1 FGF2_SHEEP	P20003 ovis aries
16	394	51.7	158	1 FGF2_CHICK	P48800 gallus gall
17	389	51.0	154	1 FGF2_MOUSE	P15655 mus musculus
18	389	51.0	154	1 FGF2_RAT	P13109 rattus norv
19	389	51.0	155	2 Q8QFR9	Q8qfr9 fugu rubrip
20	386	50.7	155	1 FGF2_HUMAN	P09038 homo sapien
21	386	50.7	196	2 P78443	P78443 homo sapien
22	386	50.7	210	2 Q7KZ72	Q7kz72 homo sapien
23	380	49.9	156	1 FGF2_MONDO	P48798 monodelphis
24	377.5	49.5	153	2 Q925A3	Q925a3 mus musculus
25	373	49.0	130	2 Q77767	Q77767 canis faml
26	370	48.6	147	1 FGF1_BRARE	Q6pbt8 brachydanio
27	364	47.8	155	1 FGF2_XENLA	P12226 xenopus lae
28	364	47.8	155	2 Q90Y52	Q90y52 cynops pyrr
29	361	47.4	137	1 FGF2_RABIT	P48799 oryctolagus
30	353	46.3	64	2 Q6LBM3	Q6lbm3 homo sapien
31	348	45.7	64	2 Q7IUP6	Q7iup6 mus musculus

32	341	44.8	170	1 FGF2_CAVPO	Q60487 cavia porce
33	327	42.9	125	2 Q88TD8	Q88td8 cynops pyrr
34	324	42.5	62	2 Q8SPL2	Q8spl2 equus caball
35	298	39.1	108	2 Q9N1S7	Q9n1s7 capreolus c
36	293	38.5	111	2 Q9BDX1	Q9bdx1 macaca mula
37	275	36.1	101	2 P79706	P79706 cynops pyrr
38	271	35.6	96	2 Q7YRNS	Q7yrns sus scrofa
39	270	35.4	105	2 Q7TPG9	Q7tpg9 mus musculus
40	258	33.9	146	2 Q076S9	Q076s9 gallus gall
41	255	33.5	211	2 Q8C7A8	Q8c7a8 mus musculus
42	253	33.2	212	2 Q9ESL9	Q9esl9 mus musculus
43	251.5	33.0	209	1 FGF9_XENLA	Q91875 xenopus lae
44	251	32.9	211	1 FGFK_HUMAN	Q9np95 homo sapien
45	250	32.8	212	2 Q9EST9	Q9est9 rattus norv

ALIGNMENTS

RESULT 1
ID FGF1_HUMAN STANDARD; PRT; 155 AA.
AC P05230; P07502;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF) (Beta-endothelial cell growth factor) (ECGF-beta).
GN Name=FGF1; Synonyms=FGFA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86261805; PubMed=3523756;
RA Jaye M., Howk R., Burgess W., Ricca G.A., Chiu I.-M., Ravera M.W., O'Brien S.J., Modi W.S., Maciag T., Drohan W.N.;
RT "Human endothelial cell growth factor: cloning, nucleotide sequence, and chromosome localization.";
RL Science 233:541-545(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain stem;
RA Wang W.P., Lehtonen K., Varban M.L., Krishnan I., Chiu I.M.;
RT "Cloning of the gene coding for human class 1 heparin-binding growth factor and its expression in fetal tissues.";
RL Mol. Cell. Biol. 9:2387-2395(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain stem;
RA Chiu I.M., Wang W.P., Lehtonen K.;
RT "Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1.";
RL Oncogene 5:755-762(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90265618; PubMed=1693186;
RA Chiu I.M., Wang W.P., Lehtonen K.;
RT "Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1.";
RL Oncogene 5:755-762(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=90073637; PubMed=2590193;
RA Merig A., Tischer E., Graves D., Tumolo A., Miller J.,
RA Gospodarowicz D., Abraham J.A., Shipley G.D., Fiddes J.C.;
RT "Structural analysis of the gene for human acidic fibroblast growth factor.";
RL Biochem. Biophys. Res. Commun. 164:1121-1129(1989).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=92019819; PubMed=1717925;
RA Wang W.P., Quick D., Balcerzak S.P., Needleman S.W., Chiu I.M.;
RT "Cloning and sequence analysis of the human acidic fibroblast growth factor gene and its preservation in leukemia patients.";
RL Oncogene 6:1521-1529(1991).

DR PDB; 1EVT; X-ray; A/B=22-155.
DR PDB; 1JQZ; X-ray; A/B=10-155.

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.5e-66;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHILQQLSAESVGVYKSTE 61
DB 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHILQQLSAESVGVYKSTE 75

QY 62 TQOYLAMTDGLLYGSGTPTNEECFLERLEENHNYTYISKHAEKNWFVGLKKGSKRG 121
DB 76 TQOYLAMTDGLLYGSGTPTNEECFLERLEENHNYTYISKHAEKNWFVGLKKGSKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 2
FGF1_MESAU
ID FGF1_MESAU STANDARD; PRT; 155 AA.
AC P34004;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1; Synonyms=FGF-1;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90270291; PubMed=1593366;
RA Hall J.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.;
RT "Characterization of the hamster DDT-1 cell aFGF/HBGF-I gene and cDNA and its modulation by steroids.";
RL J. Cell. Biochem. 43:17-26(1990).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR PIR; A60721; A60721.
DR HSSP; P05230; 1EVT.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF.FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15 By similarity.
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT DOMAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
SQ SEQUENCE 155 AA; 17403 MW; 41E5EC760B412CC5 CRC64;

Query Match 97.6%; Score 744; DB 1; Length 155;
Best Local Similarity 97.9%; Pred. No. 1.4e-64;
Matches 137; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHILQQLSAESVGVYKSTE 61

DR PDB; 1EVT; X-ray; A/B=22-155.
DR PDB; 1JQZ; X-ray; A/B=10-155.

Query Match 99.3%; Score 757; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.5e-66;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHILQQLSAESVGVYKSTE 61
DB 16 FNLPPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHILQQLSAESVGVYKSTE 75

QY 62 TQOYLAMTDGLLYGSGTPTNEECFLERLEENHNYTYISKHAEKNWFVGLKKGSKRG 121
DB 76 TQOYLAMTDGLLYGSGTPTNEECFLERLEENHNYTYISKHAEKNWFVGLKKGSKRG 135

QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSSD 155

RESULT 3
FGF1_MOUSE
ID FGF1_MOUSE STANDARD; PRT; 155 AA.
AC P61148; P10935;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1; Synonyms=FGF-1, Fgfa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201563; PubMed=2318343;
RA Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
RT "Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.";
RL Dev. Biol. 138:454-463(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97128312; PubMed=8972905; DOI=10.1016/S0378-1119(96)00365-4;
RA Madiar F., Hackshaw K.V., Chiu I.M.;
RT "Cloning and characterization of the mouse Fgf-1 gene.";
RL Gene 179:231-236(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97094746; PubMed=8939980; DOI=10.1074/jbc.271.47.30263;
RA Alam K.Y., Frostholm A., Hackshaw K.V., Evans J.E., Rotter A., Chiu I.M.;
RT "Characterization of the 1B promoter of fibroblast growth factor 1 and its expression in the adult and developing mouse brain.";
RL J. Biol. Chem. 271:30263-30271(1996).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; M30641; AAA37618.1; -.
DR EMBL; U36459; AAC52969.1; -.
DR EMBL; U36457; AAC52969.1; JOINED.
DR EMBL; U36458; AAC52969.1; JOINED.
DR EMBL; U67610; AAC52907.1; -.
DR PIR; D37360; D37360.
DR HSSP; P05230; 1EVT.
DR MGD; MGI:95515; Fgf1.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.


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CC CC EMBL; X60317; CAA42869.1; -.
DR DR PIR; JH0476; JH0476.
DR DR HSSP; P05230; LEVT.
DR DR InterPro; IPR008996; Cytok IL1 like.
DR DR InterPro; IPR022209; HB/F growthFact.
DR DR InterPro; IPR002348; IL1_HBGF.
DR DR Pfam; PF00167; FGF; 1.
DR DR PRINTS; PRO0263; HBGF_FGF.
DR DR PRINTS; PRO0262; IL1HBGF.
DR DR ProDom; PD000831; IL1_HBGF; 1.
DR DR SMART; SM00442; FGF; 1.
DR DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Direct protein sequencing; Growth factor;
KW Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 16 >152 Heparin-binding growth factor 1.
FT CHAIN 22 >152 Endothelial cell growth factor alpha.
FT CHAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
FT CONFLICT 31 31 C -> S (in Ref. 2).
FT CONFLICT 39 39 R -> Y (in Ref. 2).
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17103 MW; AE853B0A92F9ABF4 CRC64;

Query Match 95.4%; Score 727; DB 1; Length 152;
Best Local Similarity 97.8%; Pred. No. 6.2e-63;
Matches 134; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
DB 16 FNLPPGNVKKPKLLYCSNGGHFLRLPDGTGTRDRSDQHIQLQLSAESVGEVYIKSTE 75

QY 62 TQYLAMTDGLYGSQTPNECLFLERLEENHNTYISKHAENKWFVGLKNGSKRG 121
DB 76 TQYLAMTDGLYGSQTPNECLFLERLEENHNTYISKHAENKWFVGLKNGSKRG 135

QY 122 PRTHYGQKAILFLPLPV 138
DB 136 PRTHYGQKAILFLPLPV 152

RESULT 6
FGF1 BOVIN STANDARD; PRT; 155 AA.
AC AC P03958;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
DE growth factor) (aFGF) (Prostatropin) (Endothelial cell growth factor
DE beta and alpha chains) (Acidic eye-derived growth factor II) (EDGF
DE II).
GN Name=FGF1; Synonyms=AFGF, FGF-1, FGFA, HBGF-1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083506; PubMed=3205724;
RA Halley C., Courtois Y., Laurent M.;
RT "Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.";
RL Nucleic Acids Res. 16:10913-10913(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Retina;
RC MEDLINE=89078619; PubMed=2849564; DOI=10.1016/0014-5793(88)80981-5;
RA Alterio J., Halley C., Brou C., Soussi T., Courtois Y., Laurent M.;
```

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RT RT "Characterization of a bovine acidic FGF cDNA clone and its expression
RL in brain and retina.";
RN FEBS Lett. 242:41-46(1988).
RP [3]
RX SEQUENCE OF 2-155.
RA MEDLINE=87016918; PubMed=3532107;
RA Burgess W.H., Mehlman T., Marshak D.R., Fraser B.A., Maciag T.;
RT "Structural evidence that endothelial cell growth factor beta is the
RT precursor of both endothelial cell growth factor alpha and acidic
RT fibroblast growth factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:7216-7220(1986).
RP [4]
RX SEQUENCE OF 2-155.
RA MEDLINE=87026586; PubMed=3768327;
RA Crabb J.W., Ames L.G., Carr S.A., Johnson C.M., Roberts G.D.;
RT "Complete primary structure of prostatropin, a prostate epithelial
RT cell growth factor.";
RL Biochemistry 25:4988-4993(1986).
RP [5]
RX SEQUENCE OF 16-155.
RA MEDLINE=86070224; PubMed=4071057;
RA Gineez-Gallego G., Rodkey J., Bennett C., Rios-Candelore M.;
RA Disalvo J., Thomas K.;
RT "Brain-derived acidic fibroblast growth factor: complete amino acid
RT sequence and homologues.";
RL Science 230:1385-1388(1985).
RP [6]
RX SEQUENCE OF 16-44, AND AMINO-ACID COMPOSITION.
RA MEDLINE=86055750; PubMed=4065099;
RA Boehlen P., Each A., Baird A., Gospodarowicz D.;
RT "Acidic fibroblast growth factor (FGF) from bovine brain: amino-
RT terminal sequence and comparison with basic FGF.";
RL EMBO J. 4:1951-1956(1985).
RP [7]
RX SEQUENCE OF 16-56 FROM N.A.
RA MEDLINE=86261806; PubMed=2425435;
RA Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,
RA Hjerild K.A., Gospodarowicz D., Fiddes J.C.;
RT "Nucleotide sequence of a bovine clone encoding the angiogenic
RT protein, basic fibroblast growth factor.";
RL Science 233:545-548(1986).
RP [8]
RX SEQUENCE OF 16-45.
RA MEDLINE=89231704; PubMed=2714282;
RA Quinkler W., Maaberg M., Bernotat-Danielowski S., Luethke N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
RP [9]
RX SEQUENCE OF 1-18 FROM N.A.
RA Philippe J.M., Renaud F., Desset S., Laurent M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RP [10]
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA MEDLINE=91095983; PubMed=1702556;
RA Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
RA Hsu B.T., Rees D.C.;
RT "Three-dimensional structures of acidic and basic fibroblast growth
RT factors.";
RL Science 251:90-93(1991).
CC -1- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
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CC EMBL; M13439; AAA30516.1; -
CC EMBL; X13221; CAA31610.1; -
CC EMBL; X14032; CAA32192.1; -
CC EMBL; M35608; AAA30517.1; -
CC EMBL; X66446; CAA47063.1; -
CC EMBL; M97660; AAA30563.1; -
CC EMBL; M97661; AAA30564.1; -
CC PIR; JH0613; GKBOA.
CC PDB; 1AFC; X-ray; A/B/C/D/E/F/G/H=16-155.
CC PDB; 1BAR; X-ray; A/B=16-155.
CC InterPro; IPR008996; Cytok_IL1 like.
CC InterPro; IPR002209; HB/F growthfact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGFFGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC 3D-structure; Acetylation; Angiogenesis; Direct protein sequencing;
CC Growth factor; Heparin-binding; Mitogen.
CC FT PROPEP 1 15
CC FT CHAIN 2 155 Endothelial cell growth factor beta.
CC FT CHAIN 16 155 Heparin-binding growth factor 1.
CC FT CHAIN 22 155 Endothelial cell growth factor alpha.
CC FT DOMAIN 24 28 Heparin binding (Potential).
CC FT DOMAIN 113 116 Heparin binding (Potential).
CC FT MOD RES 2 2 N-acetylalanine.
CC FT TURN 23 24
CC FT STRAND 27 31
CC FT TURN 32 35
CC FT STRAND 36 37
CC FT STRAND 39 40
CC FT TURN 42 43
CC FT STRAND 45 47
CC FT TURN 52 53
CC FT TURN 56 57
CC FT STRAND 59 65
CC FT TURN 66 67
CC FT STRAND 68 73
CC FT TURN 74 76
CC FT STRAND 79 79
CC FT STRAND 82 82
CC FT TURN 84 85
CC FT STRAND 87 89
CC FT STRAND 91 91
CC FT STRAND 96 98
CC FT HELIX 100 104
CC FT TURN 106 107
CC FT STRAND 110 114
CC FT TURN 116 117
CC FT STRAND 118 120
CC FT TURN 121 121
CC FT STRAND 123 123
CC FT STRAND 126 126
CC FT TURN 128 129
CC FT STRAND 131 132
CC FT STRAND 134 134
CC FT STRAND 135 137
CC FT TURN 140 141
CC FT HELIX 143 145
CC FT STRAND 147 151
CC SQ SEQUENCE 155 AA; 17493 MW; F636641F189F9BFD CRC64;
Query Match 91.5%; Score 697; DB 1; Length 155;
Best Local Similarity 92.1%; Pred. No. 5.4e-60;
Matches 129; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 FNLPPGNYKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPLGNYKPKLLYCSNGGVFLRLPDGTVDGTRDRSDQHIQLQLSAESIGEVYIKSTE 75
Qy 62 TGOVLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVGLKKGSCRG 121
Db 76 TGOFLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVGLKKGSKLG 135
Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 PRTHFGQKAILFLPLPVSSD 155
RESULT 7
FGF1_SHEEP STANDARD; PRT; 155 AA.
AC Q7M303;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RN SEQUENCE FROM N.A.
RP PubMed=9600090; DOI=10.1006/bbrc.1998.8597;
RX Grieb T.W., Ring M., Brown E., Palmer C., Belle N., Donjerkovic D., Chang H., Yun J., Subramanian R., Forozan F., Guo Y., Vertes A., Winkles J.A., Burgess W.H.;
RA "Primary structure of ovine fibroblast growth factor-1 deduced by protein and cDNA analysis.";
RL Biochem. Biophys. Res. Commun. 246:182-191(1998).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC PIR; JH0055; JW0055.
CC InterPro; IPR002209; HB/F growthfact.
CC InterPro; IPR002348; IL1_HBGF.
CC PRINTS; PR00263; HBGFFGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC PROPEP 1 15
CC FT CHAIN 16 155 Heparin-binding growth factor 1.
CC FT DOMAIN 24 28 Heparin binding (Potential).
CC FT DOMAIN 113 116 Heparin binding (Potential).
CC SQ SEQUENCE 155 AA; 17557 MW; FE7CDEC3D35008EF CRC64;
Query Match 90.4%; Score 689; DB 1; Length 155;
Best Local Similarity 90.7%; Pred. No. 3.2e-59;
Matches 127; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Qy 2 FNLPPGNYKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FNLPLGNYKPKLLYCSNGGVFLRLPDGTVDGTRDRSDQHIQLQLSAESIGEVYIKSTE 75
Qy 62 TGOVLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVGLKKGSCRG 121
Db 76 TGOFLAMDTGCLLYGSQTPNEECFLERLEBNHYNTYISKHAENWVGLKKGSKLG 135
Qy 122 PRTHYGOKAILFLPLPVSSD 141


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Db 136 PRTHFGQKAILFLPLPVSSD 155
||||:||||:||||:||||:||||:||||:
FGF1_CHICK STANDARD; PRT; 155 AA.
AC P19596;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
DE growth factor) (aFGF) (Alpha-endothelial cell growth factor).
GN Name=FGF1; Synonyms=FGF-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91347925; PubMed=1715259;
RA Schnurch H., Risau W.;
RT "Differentiating and mature neurons express the acidic fibroblast
RT growth factor gene during chick neural development.";
RL Development 111:1143-1154(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Martin G.R., Han J.K.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 22-48.
RX MEDLINE=88296438; PubMed=3402441;
RA Rieau W., Gautschi-Sova P., Boehlen P.;
RT "Endothelial cell growth factors in embryonic and adult chick brain
RT are related to human acidic fibroblast growth factor.";
RL EMBO J. 7:959-962(1988).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
CC EMBL; S63263; AAB19629.1; -
CC EMBL; U31863; AAB80310.1; -
CC EMBL; S63261; AAD13942.1; -
CC PIR; A60130; A60130.
CC HSSP; P05230; 1EVT.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002209; HB/F_GrowthFact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGF_FGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Angiogenesis; Direct protein sequencing; Growth factor;
KW Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT BINDING 22 155 Endothelial cell growth factor alpha.

FT DOMAIN 24 28 Heparin binding (Potential).
FT DOMAIN 113 116 Heparin binding (Potential).
SQ SEQUENCE 155 AA; 17322 MW; 8EDB70545E2B4365 CRC64;

Query Match 89.0%; Score 678; DB 1; Length 155;
Best Local Similarity 90.0%; Pred. No. 3.8e-58;
Matches 126; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSASVCEVYIKSTE 61
DB 16 FGLPLGNYKKPKLLYCSNGGHFLRLPDGTVGTRDRSDQHIQLQLSADVGEVYIKSTA 75
QY 62 TGOYLAMDTGLLYGSOTPNBEECLFLERLEENHYNTYISKHAENKWFVGLKKNGSCCKRG 121
DB 76 SGQYLAMDTGLLYGSQPLGEECLFLERLEENHYNTYISKHADKNWFVGLKKNGSKLG 135
QY 122 PRTHYGQKAILFLPLPVSSD 141
DB 136 PRTHYGQKAILFLPLPVSD 155

RESULT 9
FGF1_CYNPY
ID_FGF1_CYNPY STANDARD; PRT; 148 AA.
AC Q616M7;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Fibroblast growth
DE factor 1) (FGF-1) (Acidic fibroblast growth factor) (aFGF) (Fragment).
GN Name=FGF1;
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15172893; DOI=10.1016/j.mod.2004.04.010;
RA Hayashi T., Mizuno N., Ueda Y., Okamoto M., Kondoh H.;
RT "FGF2 triggers iris-derived lens regeneration in newt eye.";
RL Mech. Dev. 121:519-526(2004).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
CC EMBL; AB175665; BAD24666.1; -
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002209; HB/F_GrowthFact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGF_FGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT NON TER 1 1
FT PROPEP <1 11 By similarity.
FT CHAIN 12 >148 Heparin-binding growth factor 1.
FT BINDING 20 24 Heparin (Potential).
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FT BINDING 109 112 Heparin (Potential).
FT NON TER 148
SQ SEQUENCE 148 AA; 16946 MW; C74C2200FCA37AD8 CRC64;
Query Match 80.3%; Score 612; DB 1; Length 148;
Best Local Similarity 82.5%; Pred. No. 1e-51; 14; Indels 0; Gaps 0;
Matches 113; Conservative 10; Mismatches 10;

Qy 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 12 FNLPGNYQRPKLLYCSNGGHFLRLPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSL 71
Qy 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYNTYISKHAEKNWVGLKKNGSKCRG 121
Db 72 TGOYLAMDSGRLYASQSPSEECFLERLEENHNYNTYISKHAEKNWVGLKKNGSKCRG 131
Qy 122 PRTHYGOKAILFLPLPV 138
Db 132 SRTHFGQKAILFLPLPV 148

RESULT 10
FGF1_XENLA STANDARD; PRT; 155 AA.
AC Q6GLR6;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (fibroblast growth
DE factor 1) (FGF-1) (Acidic fibroblast growth factor) (aFGF).
GN Name=FGF1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RG NIH - Xenopus Gene Collection (XGC) project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF (By similarity).
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
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CC -----
DR EMBL; BC074391.1; -;
DR InterPro; IPR008996; Cytok_IL1-like.
DR InterPro; IPR002209; HB/F_Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT PROPEP 1 15
FT CHAIN 16 155 Heparin-binding growth factor 1.
FT BINDING 24 28 Heparin (Potential).
FT BINDING 113 116 Heparin (Potential).
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SQ SEQUENCE 155 AA; 17318 MW; 49F5F0E465BA6597 CRC64;
Query Match 76.0%; Score 579; DB 1; Length 155;
Best Local Similarity 76.4%; Pred. No. 1.8e-48;
Matches 107; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 2 FNLPGNYKKPKLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTE 61
Db 16 FSLPIGNYKKPKLLYCSNGGVFLRLPEGVVDGTRDRNDLYITLKLALSQGEVHIKTE 75
Qy 62 TGOYLAMTDGLLYGSQTPNEECFLERLEENHNYNTYISKHAEKNWVGLKKNGSKCRG 121
Db 76 TGCYLAWDSSQLLXGTUTPNEECFLLETLEENHNYNTYISKYADNMNWFVGIKNGASKG 135
Qy 122 PRTHYGOKAILFLPLPVSSD 141
Db 136 SRTHYGOKAILFLPLPASPD 155

RESULT 11
FGF1_NOTVI STANDARD; PRT; 132 AA.
AC Q7SI8;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Heparin-binding growth factor 1 (HBGF-1) (fibroblast growth factor 1)
DE (FGF-1) (Acidic fibroblast growth factor) (aFGF) (Fragment).
GN Name=FGF1;
OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notoththalmus.
OX NCBI_TaxID=8316;
RN [1]
RP STRUCTURE BY NMR.
RA Arunkumar A.I., Srisaillam S., Kumar T.K.S., Chiu I.M., Yu C.;
RL Submitted (AUG-2000) to the PDB data bank.
CC -1- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF (By similarity).
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC PDB; 1FMM; NMR; S=1-132.
DR InterPro; IPR008996; Cytok_IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; IL1_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW 3D-structure; Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT NON_TER 1 1
FT BINDING 1 5 Heparin (Potential).
FT BINDING 90 93 Heparin (Potential).
SQ SEQUENCE 132 AA; 15015 MW; 76CABAF337B29C7B CRC64;
Query Match 74.9%; Score 571; DB 1; Length 132;
Best Local Similarity 81.1%; Pred. No. 8.8e-48;
Matches 107; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 10 KKPCLLYCSNGGHFLRLPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTEQYLAMD 69
Db 1 QKPCLLYCSNGGVFLRLFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLTQYLAMD 60
Qy 70 TDGLLYGSQTPNEECFLERLEENHNYNTYISKHAEKNWVGLKKNGSKCRGPRTHYGOK 129
Db 61 SDGLLYASQSPSEECFLERLEENHNYNTYISKVHADKDWFGVGIKNGKTPGSRTHFGOK 120
Qy 130 AILFLPLPVSSD 141
Db 121 AILFLPLPVSSD 132
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RESULT 12
FGF1_CAPCA STANDARD; PRT; 106 AA.
AC Q9N1S8;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Fibroblast growth factor 1)
DE (FGF-1) (Acidic fibroblast growth factor) (aFGF) (Fragment).
GN Name=FGF1;
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20532861; PubMed=11078967; DOI=10.1016/S0378-4320(00)00191-3;
RA Wagener A., Blotner S., Goritz F., Fickel J.;
RT "Detection of growth factors in the testis of roe deer (Capreolus capreolus).";
RL Anim. Reprod. Sci. 64:65-75(2000).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: This protein binds heparin, although less strongly
CC than does bFGF (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF152586; AAF73225.1; -.
DR HSP; P05230; IJQZ.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Growth factor; Heparin-binding; Mitogen.
FT NON_TER 1
FT BINDING 83 86 Heparin (Potential).
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11931 MW; 2EEC9C1D749A5023 CRC64;

Query Match 69.4%; Score 529; DB 1; Length 106;
Best Local Similarity 91.5%; Pred. No. 8.5e-44;
Matches 97; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 17 CSNGGHFLRLPDGTGDRSDQHILQLSAESVGEVYIKSTGTGQYLAAMDTDGLLYG 76
DQ 1 CRNGGHFLRLPDGTGDRSDQHILQLSAESVGEVYIKSTGTGQYLAAMDTDGLLYG 60

QY 77 SQTPEECFLERLEENHYNTYISKHAEKQWVGLKKNKSGCKRGP 122
DQ 61 SQTPEECFLERLEENHYNTYISKHAEKQWVGLKKNKSGCKRGP 106

RESULT 13
FGF2_BOVIN STANDARD; PRT; 155 AA.
AC P03969;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast
DE growth factor) (BFGF) (Prostatropin) (Contains: Kidney-derived growth
DE factor).
GN Name=FGF2; Synonyms=FGF-2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86261806; PubMed=2425435;
RA Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,
RA Hjerild K.A., Gospodarowicz D., Fiddes J.C.;
RT "Nucleotide sequence of a bovine clone encoding the angiogenic
```

protein, basic fibroblast growth factor.";

[2]

RL Science 233:545-548(1986).

RP SEQUENCE FROM N.A.

RX MEDLINE=87217066; PubMed=3472745;

RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

RT "Human basic fibroblast growth factor: nucleotide sequence, genomic organization, and expression in mammalian cells.";

RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).

[3]

RP SEQUENCE OF 10-155.

RX MEDLINE=86016731; PubMed=3863109;

RA Esch F., Baird A., Ling N., Ueno N., Hill F., Denoroy L., Klepper R., Gospodarowicz D., Boehlen P., Guillemin R.;

RT "Primary structure of bovine pituitary basic fibroblast growth factor (FGF) and comparison with the amino-terminal sequence of bovine brain acidic FGF.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:6507-6511(1985).

[4]

RP SEQUENCE OF 1-9.

RX MEDLINE=86295737; PubMed=3741423;

RA Ueno N., Baird A., Esch F., Ling N., Guillemin R.;

RT "Isolation of an amino terminal extended form of basic fibroblast growth factor.";

RL Biochem. Biophys. Res. Commun. 138:580-588(1986).

[5]

RP SEQUENCE OF 10-23 AND 25-38.

RX TISSUE=Adrenal gland;

RX PubMed=3940857;

RA Gospodarowicz D., Baird A., Cheng J., Lui G.M., Esch F., Bohlen P.;

RT "Isolation of fibroblast growth factor from bovine adrenal gland: physicochemical and biological characterization.";

RL Endocrinology 118:82-90(1986).

[6]

RP SEQUENCE OF 12-24.

RX TISSUE=Pituitary;

RX PubMed=6591194;

RA Bohlen P., Baird A., Esch F., Ling N., Gospodarowicz D.;

RT "Isolation and partial molecular characterization of pituitary fibroblast growth factor.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5364-5368(1984).

[7]

RP SEQUENCE OF 14-33.

RX PubMed=3596000;

RA Bertolini J., Hearn M.T.;

RT "Isolation, characterization and tissue localisation of an N-terminal-truncated variant of fibroblast growth factor.";

RL Mol. Cell. Endocrinol. 51:187-199(1987).

[8]

RP SEQUENCE OF 25-41.

RX TISSUE=Kidney;

RX MEDLINE=86095426; PubMed=4081126; DOI=10.1016/0167-0115(85)90061-8;

RA Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;

RT "Isolation and partial characterization of an endothelial cell growth factor from the bovine kidney: homology with basic fibroblast growth factor.";

RL Regul. Pept. 12:201-213(1985).

[9]

RP SEQUENCE OF 21-40.

RX TISSUE=Kidney;

RX MEDLINE=87119165; PubMed=3809608; DOI=10.1016/0167-0115(86)90057-1;

RA Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Guillemin R.;

RT "Purification and partial characterization of a mitogenic factor from bovine liver: structural homology with basic fibroblast growth factor.";

RL Regul. Pept. 16:135-145(1986).

[10]

RP SEQUENCE OF 25-39.

RX TISSUE=Testis;

RX PubMed=3556754;

RA Ueno N., Baird A., Esch F., Ling N., Guillemin R.;

RT "Isolation and partial characterization of basic fibroblast growth factor from bovine testis.";

RL Mol. Cell. Endocrinol. 49:189-194(1987).

CC -|- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.

CC -|- SUBUNIT: Monomer.

CC -|- MISCELLANEOUS: This protein binds heparin more strongly than does aFGF.

CC -|- SIMILARITY: Belongs to the heparin-binding growth factors family.

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CC -----

DR EMBL; M13440; AAA30518.1; -.

DR PIR; A24663; GKEOB.

DR HSSP; P09038; 1BFF.

DR InterPro; IPR008996; Cytok IL1 like.

DR InterPro; IPR002209; HB/F_Growthfact.

DR InterPro; IPR002348; IL1_HBGF.

DR Pfam; PF00167; FGF; 1.

DR PRINTS; PR00263; HBGF.FGF.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD000831; IL1_HBGF; 1.

DR SMART; SM00442; FGF; 1.

DR PROSITE; PS00247; HBGF_FGF; 1.

DR Angiogenesis; Direct protein sequencing; Growth factor;

KW Heparin-binding; Mitogen.

FT PROPEP 1 9

FT CHAIN 10 155 Heparin-binding growth factor 2.

FT CHAIN 25 155 Kidney-derived growth factor.

FT DOMAIN 27 31 Heparin binding (Potential).

FT DOMAIN 116 119 Heparin binding (Potential).

FT SITE 46 48 Cell attachment site (atypical) (Potential).

FT SITE 88 90 Cell attachment site (atypical) (Potential).

FT SITE 90 90 Cell attachment site (atypical) (Potential).

SQ SEQUENCE 155 AA; 17250 MW; BE6CE70FA6107129 CRC64;

Query Match 51.8%; Score 395; DB 1; Length 155;

Best Local Similarity 56.6%; Pred. No. 1.6e-30;

Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;

Qy 5 PPGNYKPKLLYCSNGGHFLRILPDGTVGTRDRSDQHIQLQSAESVGEVYIKSTETGQ 64

Db 22 PGHFHDKPKLYCKNGGFFLRIPHGRVDRGVRKSDPHIKLQLQAEERGVVSIKGVCANR 81

Qy 65 YLAMDTGLLYGSGTPNEECFLERLEENHYNTYISKHAEKNWFGVGLKNGSKCRGPRT 124

Db 82 YLAMKEDGLRLASCKVTDCEFFERLESNNYNTYRSRKYSSWYALKRTGYKLGPKT 139

Qy 125 HYGOKAILFLPLPVSS 140

Db 140 GPGOKAILFLPMSAKS 155

RESULT 15

1D_FGF2 SHEEP

1D_FGF2 SHEEP STANDARD; PRT; 155 AA.

AC P20003;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).

DE Name=FGF2; Synonyms=FGF-2;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RL Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RN Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 9-155.
RX MEDLINE=88055577; PubMed=3678486; DOI=10.1016/0014-5793(87)80435-0;
RA Simpson R.J., Moritz R.L., Lloyd C.J., Fabri L.J., Nice E.C.,
RA Rubira M.R., Burgess A.W.;
RT "Primary structure of ovine pituitary basic fibroblast growth
RT factor.";
RL FEBS Lett. 224:128-132(1987).
CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
CC in vivo and are potent mitogens for a variety of cell types in
CC vitro. There are differences in the tissue distribution and
CC concentration of these 2 growth factors.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: This protein binds heparin more strongly than does
CC aFGF.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36136; AAA31519.1; -.
DR HSSP; P09038; 1BFF.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR002209; HB/F Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SMO0442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Angiogenesis; Direct protein sequencing; Growth factor;
KW Heparin-binding; Mitogen.
FT PROPEP 1 9
FT CHAIN 10 155 Heparin-binding growth factor 2.
FT DOMAIN 27 31 Heparin binding (Potential).
FT DOMAIN 116 119 Heparin binding (Potential).
FT SITE 46 48 Cell attachment site (atypical)
FT SITE 88 90 (Potential).
FT SITE Cell attachment site (atypical)
FT (Potential).
SQ SEQUENCE 155 AA; 17280 MW; B5F2364BA610606D CRC64;

Query Match 51.8%; Score 395; DB 1; Length 155;
Best Local Similarity 56.6%; Fred. No. 1.6e-30;
Matches 77; Conservative 17; Mismatches 40; Indels 2; Gaps 1;

QY 5 PPGNYKPKLLYCSNGHFLRILPDGTVDGTRDRSDQHQLQLSAESVGEVYIKSTGTGQ 64
DB 22 PPGHFKDPRLYCKNGGFFLIHPDGRVDGVRKSDPHIKLQQAEEGVVSIKGVCANR 81
QY 65 YLAMDTGLLYGSGTPNECLFLERLENNHYNTYISKHAENKWNFVLKKNKSGCKRGPT 124
DB 82 YLAWKEDGRLLASKCVTDCCFFERLESNNYNTYRSKYS--SWYVALKRTGYKLGPKT 139
QY 125 HYGQKAILFLPVSS 140
DB 140 GPGQKAILFLPMSAKS 155

Search completed: June 6, 2005, 07:41:33
Job time : 108.179 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	630	100.0	630	6	ABK10595	Abk10595 CDNA enco
2	630	100.0	630	6	AAK98920	AAk98920 Codon opt
3	630	100.0	630	12	ADO55205	Ado55205 Human aci
4	584	92.7	630	6	ABK10594	Abk10594 CDNA enco
5	584	92.7	630	6	AAK98919	AAk98919 Codon opt
6	584	92.7	630	12	ADO55203	Ado55203 Human aci
7	567.4	90.1	990	6	AAK98922	AAk98922 Codon opt
8	536	85.1	630	6	ABK10592	Abk10592 CDNA enco
9	536	85.1	630	6	AAK98917	AAk98917 Codon opt
10	536	85.1	630	12	ADO55200	Ado55200 Human aci
11	341.6	54.2	8501	2	AAK12907	AAk12907 Novel exp
12	290	46.0	454	2	AAQ02421	AAq02421 CDNA enco
13	290	46.0	454	2	AAQ03873	AAq03873 Synthetic
14	290	46.0	454	2	AAQ10399	AAq10399 Human aci
15	290	46.0	454	2	AAQ10166	AAq10166 Human aci
16	290	46.0	454	2	AAQ25916	AAq25916 aFGF mute
17	288.8	45.8	496	2	AAQ03871	AAq03871 Synthetic
18	286.8	45.5	440	1	AAK90117	AAk90117 Human aci
19	285.4	45.3	490	11	ADJ32064	Adj32064 Human cDN
20	285.4	45.3	638	1	AAK07888	AAk07888 Complete

Producing a biologically active human acidic fibroblast growth factor (haFGF) protein for use in promoting angiogenesis, involves employing an *E. coli* transformed with a plasmid having an haFGF gene operably linked to a promoter.

Disclosure; Fig 8; 41pp; English.

Db 421 GAAAAAATCATGAGAGAGAACTGGTTTCTAGGCGCTTAAAAAATGGTTCTCTGTAAGCG 480
 Qy 481 TGGACCAACGAGTCACTATGCGCAAGAGCTATCTGTTCCTGCGCACTACCACTGAGCTC 540
 Db 481 TGGACCAACGAGTCACTATGCGCAAGAGCTATCTGTTCCTGCGCACTACCACTGAGCTC 540
 Qy 541 CGACTAAGAGTCCGAATTCGAGCTCGTGCACAAGCTTCGCGCGGCGCACTCGAGCACCCACC 600
 Db 541 CGACTAAGAGTCCGAATTCGAGCTCGTGCACAAGCTTCGCGCGGCGCACTCGAGCACCCACC 600
 Qy 601 ACCACCACTGAGATCCGGTGTCTAACA 630
 Db 601 ACCACCACTGAGATCCGGTGTCTAACA 630

RESULT 4
 ID ABK10594 standard; cDNA; 630 BP.
 AC ABK10594;
 XX
 DT 05-JUN-2002 (first entry)
 DE cDNA encoding human acidic FGF protein (hAFGF134).
 KW hAFGF134; acidic fibroblast growth factor; cell proliferation;
 KW differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
 KW ss; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..529
 FT /*tag= a
 FT /product= "hAFGF 134 protein"
 XX
 WO200214471-A2.
 XX
 XX
 PD 21-FEB-2002.
 XX
 PF 15-AUG-2001; 2001WO-US025537.
 XX
 PR 15-AUG-2000; 2000US-0225406P.
 XX
 PA (PHAG-) PHAGE BIOTECHNOLOGY CORP.
 XX
 PI Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
 DR WPI: 2002-257598/30.
 DR N-PSDB; AAU76944.
 XX
 PT Producing a biologically active human acidic fibroblast growth factor
 PT (hAFGF) protein for use in promoting angiogenesis, involves employing an
 PT E. coli transformed with a plasmid having an hAFGF gene operably linked
 PT to a promoter.
 XX
 PS Example 1; Fig 6; 41pp; English.

This invention relates to a novel method for producing a biologically active human acidic fibroblast growth factor (hAFGF) protein. Fibroblast growth factors are potent regulators of cell proliferation, differentiation and normal development and they have been shown to play a role in tumorigenesis and metastasis. Acidic fibroblast growth factor has been shown to be potent inducers of angiogenesis. The gene for acidic fibroblast growth factor is located on human chromosome 5. The method of the invention comprises employing a plasmid having at least one copy of the gene, which encodes a biologically active hAFGF protein operably linked to a promoter, to transform *Escherichia coli*. The method is useful for producing recombinant or biologically active hAFGF protein, which is useful in promoting angiogenesis. The present sequence represents a cDNA encoding the human acidic fibroblast growth factor 134 protein (hAFGF134) used in the method of the invention. This sequence has been chemically

CC synthesised using the codons which are most often used by *E. coli*, to
 CC facilitate its expression
 XX
 SQ Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
 Query Match 92.7%; Score 584; DB 6; Length 630;
 Best Local Similarity 97.1%; Pred. No. 5.1e-147;
 Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
 QY 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCACTATAGGGAATTGT 60
 Db 1 GCGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTCACTATAGGGAATTGT 60
 QY 61 GAGCGGATAACAATTCCTCTAGAAATAATTTGTTTAACTTTAAGAGAGATATACA 120
 Db 61 GAGCGGATAACAATTCCTCTAGAAATAATTTGTTTAACTTTAAGAGAGATATACA 120
 QY 121 TATGTTTAACTTCGCGCGGGAATTAACAAAAACCCCAAGCTTCTTTACTCAGTAACGG 180
 Db 121 TAT-----GAATTACAAAAACCCCAAGCTTCTTTACTCAGTAACGG 162
 QY 181 AGGACATTTCTGCGAATTTGCGAGATGGCAAGTAGATGGGACTCGCGATCGCTCCGA 240
 Db 163 AGGACATTTCTGCGAATTTGCGAGATGGCAAGTAGATGGGACTCGCGATCGCTCCGA 222
 QY 241 CCAGCACATTGAGTGGCAACTCTCGCGGAAAGCGTTGGAGAGGTCTATATCAAGTCCAC 300
 Db 223 CCAGCACATTGAGTGGCAACTCTCGCGGAAAGCGTTGGAGAGGTCTATATCAAGTCCAC 282
 QY 301 GGAGATGGCCAGTACCTTGGCATGGGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 360
 Db 283 GGAGATGGCCAGTACCTTGGCATGGGACACCGATGGGCTTCTGTATGGCTCACAGACGCC 342
 QY 361 TAAAGAGAAATGCTTTTCTAGAAAGACTAGAGAAACCATTTACAAACAGTACATATC 420
 Db 343 TAAAGAGAAATGCTTTTCTAGAAAGACTAGAGAAACCATTTACAAACAGTACATATC 402
 QY 421 GAAAAACATGCAGAGAGAACTGGTTTGTAGGCGCTTAAAAAATGGTTCTCTGTAAGCG 480
 Db 403 GAAAAACATGCAGAGAGAACTGGTTTGTAGGCGCTTAAAAAATGGTTCTCTGTAAGCG 462
 QY 481 TGGACCAACGAGTCACTATGCGCAAGAGCTATCTTTCTGCGCACTACCACTGAGCTC 540
 Db 463 TGGACCAACGAGTCACTATGCGCAAGAGCTATCTTTCTGCGCACTACCACTGAGCTC 522
 QY 541 CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGGCGCACTCGAGCACCCACC 600
 Db 523 CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGGCGCACTCGAGCACCCACC 582
 QY 601 ACCACCACTGAGATCCGGCTGTACA 630
 Db 583 ACCACCACTGAGATCCGGCTGTACA 612

RESULT 5
 AAK98919
 ID AAK98919 standard; DNA; 630 BP.
 XX
 AC AAK98919;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Codon optimised DNA of chemically synthesised human A FGF (134AA).
 XX
 KW Human acidic fibroblast growth factor; phage T7 polymerase promoter;
 KW lysis; phage dependent superproduction; A FGF; codon optimisation; gene;
 KW ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..529

```

FT      /*tag= a
FX      /product= "Protein of human A FGF (134AA)"
FN      WO200214468-A2.
XX      21-FEB-2002.
PD      15-AUG-2001; 2001WO-US025477.
XX      15-AUG-2000; 2000US-0225437P.
PF      (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX      Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX      WPI; 2002-269184/31.
DR      P-PSDB; AAO19991.
XX      Bacteriophage-dependent method for producing biologically active proteins
XX      or peptides, involves employing an Escherichia coli transformed with a
XX      plasmid containing the targeted gene(s) operably linked to a promoter.
PS      Example 2; Fig 6; 44pp; English.
XX      The invention relates to a method for enhancing the production of a
XX      biologically active protein comprising infecting a strain of Escherichia
XX      coli, which has been transformed with a plasmid having at least one copy
XX      of an expressible gene, such as a human acidic fibroblast growth factor.
XX      The expressible gene encodes a biologically active protein operably
XX      linked to a phase T7 polymerase promoter, with a bacteriophage capable of
XX      mediating delayed lysis. The method is useful for the phase dependent
XX      superproduction of biologically active protein and peptides. The method
XX      is particularly useful for enhancing the production of heterologous
XX      proteins in bacterial host cells. This polynucleotide sequence represents
XX      a codon optimised DNA of a chemically synthesised human acidic fibroblast
XX      growth factor - human A FGF (134AA) of the invention
XX      Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
SQ      Query Match          92.7%; Score 584; DB 6; Length 630;
          Best Local Similarity 97.1%; Pred. No. 5.1e-147;
          Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
QY      1 GCCTAGAGATCGAGATCTCGATCCGCGGAAATTAATACGACTCATTATAGGGGAATTGT 60
DB      1 GCCTAGAGATCGAGATCTCGATCCGCGGAAATTAATACGACTCATTATAGGGGAATTGT 60
QY      61 GAGCGGATACAAATCCCTCTAGAAATAATTTTGTAACTTTAAGAGGAGATATACA 120
DB      61 GAGCGGATACAAATCCCTCTAGAAATAATTTTGTAACTTTAAGAGGAGATATACA 120
QY      121 TATGTTTAACTTTCCGCGCGGAAATTAACAAACCAACCAAGCTTTCTTACTGCGATACGG 180
DB      121 TAT-----GAAATTAACAAACCAACCAAGCTTTCTTACTGCGATACGG 162
QY      181 AGGACATTTCTGCGAATTTCTGCAGATGGGACAGTAGATGGGATCGCGATCGCTCCGA 240
DB      163 AGGACATTTCTGCGAATTTCTGCAGATGGGACAGTAGATGGGATCGCGATCGCTCCGA 222
QY      241 CCAGCATTTCTGCGAATTTCTGCAGATGGGACAGTAGATGGGATCGCTCAAGTCGAC 300
DB      223 CCAGCATTTCTGCGAATTTCTGCAGATGGGACAGTAGATGGGATCGCTCAAGTCGAC 282
QY      301 GGAGCTGGGCGAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCC 360
DB      283 GGAGCTGGGCGAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCC 342
QY      361 TAACGAAGAATGCTTTGTTTCTAGAAAGACTAGAGAGAAAACATTAACACGATACATC 420
DB      343 TAACGAAGAATGCTTTGTTTCTAGAAAGACTAGAGAGAAAACATTAACACGATACATC 402
QY      421 GAAAAACATGCAGAGAAAGACTGGTTGTAGGCTTTAAAAAATGTTCTTCTAGAGC 480

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DB      403 GAAAAAACATCGAGAGAGAACTGGTTTGTAGGCTTTAAAAAATGTTCTCTAGAGG 462
QY      481 TGGACACGGAATCTACTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCACTGAGCTC 540
DB      463 TGGACACGGAATCTACTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCACTGAGCTC 522
QY      541 CGACTAAGGATCCGAATTCGAGCTCCGTCGACAGACTTGGCGCGGCGACTCGAGACCAACC 600
DB      523 CGACTAAGGATCCGAATTCGAGCTCCGTCGACAGACTTGGCGCGGCGACTCGAGACCAACC 582
QY      601 ACCACCACTGAGATCCGGCTGCTAACA 630
DB      583 ACCACCACTGAGATCCGGCTGCTAACA 612

RESULT 6
AD055203
ID      AD055203 standard; DNA; 630 BP.
AC      AD055203;
XX      09-SEP-2004 (first entry)
DT      Human acidic fibroblast growth factor (hAFGF) DNA seqid 4.
XX      neoangiogenesis stimulator; cardiant; vasotropic; revascularisation;
XX      ischaemic region; fibroblast growth factor-1; FGF-1; neoangiogenesis;
XX      acidic FGF; aFGF; bacteriophage lambda; coronary artery disease;
XX      myocardial perfusion; revascularisation therapy; ischaemic myocardium;
XX      human; gene; ds.
XX      Homo sapiens.
XX      Synthetic.
OS      Key
FH      122. .529
CDS      /*tag= a
          /product= "hAFGF"
          /note= "human acidic fibroblast growth factor"
US2004115769-A1.
XX      17-JUN-2004.
XX      27-AUG-2003; 2003US-00649480.
PF      24-JUL-1998; 98US-0093962P.
XX      22-JUL-1999; 99US-00358780.
PR      15-AUG-2000; 2000US-0225406P.
PR      15-AUG-2001; 2001US-00929945.
XX      (STEG/) STEGMANN T J.
PA      (KORD/) KORDYUM V A.
PA      (SLAV/) SLAVCHENKO I Y.
PA      (CHER/) CHERNYKH S I.
PA      (VOZI/) VOZIANOV O F.
XX      Stegmann TJ, Kordyum VA, Slavchenko IY, Chernykh SI, Vozianov OF;
XX      WPI; 2004-449397/42.
XX      Revascularizing an ischemic region, for treating coronary artery disease,
XX      comprises preparing and injecting a composition comprising a recombinant
XX      human fibroblast growth factor-1 into the ischemic region to induce local
XX      neoangiogenesis.
PS      Claim 2; SEQ ID NO 4; 42pp; English.
XX      The invention describes revascularising an ischaemic region comprising
XX      preparing a pharmaceutical composition comprising a recombinant
XX      fibroblast growth factor-1 (FGF-1) and injecting an amount of the
XX      pharmaceutical composition into the ischaemic region, the amount being
XX      sufficient to induce local neoangiogenesis. The FGF-1 is prepared by

```

transforming an Escherichia coli host cell with a plasmid comprising an expressible gene encoding a biologically active human acidic FGF protein, operably linked to a promoter; infecting the transformed bacterial host cell with a bacteriophage ϕ lg; which mediates delayed lysis; and culturing the E. coli host cell under a culture condition that induces lytic growth of the cell without lysis until a desired level of production of the protein is reached, where the protein is produced as a soluble, biologically-active human acidic FGF protein. Also described is a method of treating coronary artery disease in a patient, comprising preparing a pharmaceutical composition comprising a recombinant FGF-1; injecting an amount of the pharmaceutical composition into at least one site in a heart wall, the amount being sufficient to improve myocardial perfusion; and injecting a composition comprising a physiological glue to a surface of the heart at the site(s) where the pharmaceutical composition was injected. The methods are useful for treating coronary heart disease by revascularisation therapy or for inducing local neovascularisation in ischaemic myocardium. This sequence represents human acidic fibroblast growth factor (hAFGF) DNA which has been modified by substitution of naturally occurring codons with codons found in highly expressed E.coli proteins.

Sequence 630 BP; 193 A; 158 C; 145 G; 134 T; 0 U; 0 Other;
 Query Match 92.7%; Score 584; DB 12; Length 630;
 Best Local Similarity 97.1%; Pred. No. 5.1e-147;
 Matches 612; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

QY 1 GCGTAGAGATCGAGATCTCGATCCCGGAAATTAATACGATCACTATAGGGGAATTGT 60
 DB |||||
 QY 1 GCGTAGAGATCGAGATCTCGATCCCGGAAATTAATACGATCACTATAGGGGAATTGT 60
 DB |||||
 QY 61 GAGCGGATAACAAATCCCTCTAGAAATATTTGTTTAACTTTAAGAGGAGATATACA 120
 DB |||||
 QY 61 GAGCGGATAACAAATCCCTCTAGAAATATTTGTTTAACTTTAAGAGGAGATATACA 120
 DB |||||
 QY 121 TATGTTTAACTTCCGCGCGGAAATACAAAAAACCAGCTTCTTTACTGCGAGTAAACGG 180
 DB |||||
 QY 121 TAT-----GAAATACAAAAAACCAGCTTCTTTACTGCGAGTAAACGG 162
 DB |||||
 QY 181 AGGACACTTCTCGGAATTTCTCCAGATGGCACAGTAGATGGGATCGCGATCGCTCCGA 240
 DB |||||
 QY 163 AGGACACTTCTCGGAATTTCTCCAGATGGCACAGTAGATGGGATCGCGATCGCTCCGA 222
 DB |||||
 QY 241 CCAGCACATTCAGTCGCAACTCCGCGGAAAGCGTTGAGAGGTCATATCAAGTCGAC 300
 DB |||||
 QY 223 CCAGCACATTCAGTCGCAACTCCGCGGAAAGCGTTGAGAGGTCATATCAAGTCGAC 282
 DB |||||
 QY 301 GGAGACTGCCAGTACTTGGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCC 360
 DB |||||
 QY 283 GGAGACTGCCAGTACTTGGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCC 342
 DB |||||
 QY 361 TAAAGGAAGATGCTTGTCTTCTAGAAAGACTAGAAAGAAACCAATTAACACATCATATC 420
 DB |||||
 QY 343 TAAAGGAAGATGCTTGTCTTCTAGAAAGACTAGAAAGAAACCAATTAACACATCATATC 402
 DB |||||
 QY 421 GAAAGACATGAGAGAGAACTGTTTCTAGGCTTAAAGAAATGTTCTCTGTAAGCG 480
 DB |||||
 QY 403 GAAAGACATGAGAGAGAACTGTTTCTAGGCTTAAAGAAATGTTCTCTGTAAGCG 462
 DB |||||
 QY 481 TGGACCAAGGACTCACTATGGCCAAAGGCTATCTGTCTCGCCACTACAGTGGCTC 540
 DB |||||
 QY 463 TGGACCAAGGACTCACTATGGCCAAAGGCTATCTGTCTCGCCACTACAGTGGCTC 522
 DB |||||
 QY 541 CGACTAAGGATCCGAATTCGAGCTCGTCGACAAAGCTTCGCGCGGACCTCGAGCACACC 600
 DB |||||
 QY 523 CGACTAAGGATCCGAATTCGAGCTCGTCGACAAAGCTTCGCGCGGACCTCGAGCACACC 582
 DB |||||
 QY 601 ACCACCACTGAGATCCGGCTGTAAACA 630
 DB |||||
 QY 583 ACCACCACTGAGATCCGGCTGTAAACA 612
 DB |||||

AAK98922
 ID AAK98922 standard; DNA; 990 BP.
 AC AAK98922;
 DT 24-MAY-2002 (first entry)
 DE Codon optimised synthetic gene encoding human interferon alpha-2b.
 KW Human acidic fibroblast growth factor; phase T7 polymerase promoter; lysis; phase dependent superproduction; synthetic; growth hormone; gene; human interferon alpha-2b; codon optimisation; ds.
 OS Homo sapiens.
 XX Synthetic.
 FH Key Location/Qualifiers
 FT promoter 231..249 /*tag= b
 FT misc_signal 250..274 /*tag= c
 FT /note= "Operator sequence"
 FT CDS 320..787 /*tag= a
 FT /product= "Protein of a human interferon alpha-2b"
 XX WO200214468-A2.
 XX 21-FEB-2002.
 PF 15-AUG-2001; 2001WO-US025477.
 PR 15-AUG-2000; 2000US-0225437P.
 XX (PHAG-) PHAGE BIOTECHNOLOGY CORP.
 XX Kordyum VA, Chernykh SI, Slavchenko IV, Vozianov OF;
 XX WPI; 2002-269184/31.
 DR P-PSDB; AAO19994.
 XX Bacteriophage-dependent method for producing biologically active proteins or peptides, involves employing an Escherichia coli transformed with a plasmid containing the targeted gene(s) operably linked to a promoter.
 XX Example 8; Fig 10; 44pp; English.
 XX The invention relates to a method for enhancing the production of a biologically active protein comprising infecting a strain of Escherichia coli, which has been transformed with a plasmid having at least one copy of an expressible gene, such as a human acidic fibroblast growth factor. The expressible gene encodes a biologically active protein operably linked to a phase T7 polymerase promoter, with a bacteriophage capable of mediating delayed lysis. The method is useful for the phage dependent superproduction of biologically active protein and peptides. The method is particularly useful for enhancing the production of heterologous proteins in bacterial host cells. This polynucleotide sequence represents a codon optimised synthetic gene encoding human interferon alpha-2b of the invention
 XX Sequence 990 BP; 275 A; 262 C; 239 G; 214 T; 0 U; 0 Other;
 Query Match 90.1%; Score 567.4; DB 6; Length 990;
 Best Local Similarity 92.8%; Pred. No. 1.7e-142;
 Matches 623; Conservative 0; Mismatches 6; Indels 42; Gaps 1;
 QY 2 CGTAGAGATCGAGATCTCGATCCCGGAAATTAATACGATCACTATAGGGGAATTGTG 61
 DB 200 CGTGGCGCCGAGATCTCGATCCCGGAAATTAATACGATCACTATAGGGGAATTGTG 259
 QY 62 AGCGGATAACAAATTCCTCTCTAGAAATTAATTTGTTTAACTTTAAGAGGAGATATACAT 121
 DB 260 AGCGGATAACAAATTCCTCTCTAGAAATTAATTTGTTTAACTTTAAGAGGAGATATACAT 319

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QY 122 ATG-----TTTAACTTCGCCC 139
DB 320 ATGGCTGAAGGGAAATCAACACCTTTACAGCGTTAAACCGAGAAATTTAACTTCGCCC 379
QY 140 GGGAAATTACAAAAACCCAAAGCTTCTTTACTGAGTAACGGAGGACATCTCTCGGAATT 199
DB 380 GGGAAATTACAAAAACCCAAAGCTTCTTTACTGAGTAACGGAGGACATCTCTCGGAATT 439
QY 200 CTGCCAGATGGCACTAGATGGGACTCGCGATCGCTCCGACAGACATTCAGCTGCAA 259
DB 440 CTGCCAGATGGCACAGTATGGGACTCGCGATCGCTCCGACAGACATTCAGCTGCAA 499
QY 260 CTCTCGCGAAAGCGTTGGAGAGGCTTATATCAAGTCGACCGAGACTGCGCACTACCTT 319
DB 500 CTCTCGCGAAAGCGTTGGAGAGGCTTATATCAAGTCGACCGAGACTGCGCACTACCTT 559
QY 320 GCCATGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATCTTTGTTT 379
DB 560 GCCATGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAACGAAAGATCTTTGTTT 619
QY 380 CTAGAAGACTAGAGAAACCAATTACAACCTATATCGAAAAACATGACAGAGAG 439
DB 620 CTAGAAGACTAGAGAAACCAATTACAACCTATATCGAAAAACATGACAGAGAG 679
QY 440 AACTGGTTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACCGGACTCACTAT 499
DB 680 AACTGGTTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACCGGACTCACTAT 739
QY 500 GGCCAAAGGCTATCTTTCTCCGCACTACCACTGAGCTCCGACTAAGGATCCGAATTC 559
DB 740 GGCCAAAGGCTATCTTTCTCCGCACTACCACTGAGCTCCGACTAAGGATCCGAATTC 799
QY 560 GAGCTCCGTCGACAAAGCTTGGCGCGCACTCGAGCACACCAACCAACCACTGAGATCC 619
DB 800 GAGCTCCGTCGACAAAGCTTGGCGCGCACTCGAGCACACCAACCAACCACTGAGATCC 859
QY 620 GGCTGCTAACA 630
DB 860 GGCTGCTAACA 870

RESULT 8
ID ABK10592 standard; cDNA; 630 BP.
AC ABK10592;
DE 05-JUN-2002 (first entry)
KW cDNA encoding human acidic FGF protein HAFGF155.
KW HAFGF155; acidic fibroblast growth factor; cell proliferation;
KW differentiation; tumorigenesis; metastasis; angiogenesis; chromosome 5;
KW ss; human.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 122..589
FT /*tag= a
FT /product= "HAFGF 155 protein"
XX WO200214471-A2.
XX PD 21-FEB-2002.
XX PF 15-AUG-2001; 2001WO-US025537.
XX PR 15-AUG-2000; 2000US-0225406P.
XX PH (PHAG-) PHAGE BIOTECHNOLOGY CORP.
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XX Stegmann TJ, Kordyum VA, Chernykh SI, Slavchenko IV, Vorizanov OF;
PI WPI: 2002-257598/30.
DR P-PSDB; AAU6943.
XX Producing a biologically active human acidic fibroblast growth factor
PT (hAFGF) protein for use in promoting angiogenesis, involves employing an
PT E. coli transformed with a plasmid having an hAFGF gene operably linked
PT to a promoter.
XX Example 1; Fig 1; 41pp; English.
XX This invention relates to a novel method for producing a biologically
CC active human acidic fibroblast growth factor (hAFGF) protein. Fibroblast
CC growth factors are potent regulators of cell proliferation,
CC differentiation and normal development and they have been shown to play a
CC role in tumorigenesis and metastasis. Acidic fibroblast growth factor
CC has been shown to be potent inducers of angiogenesis. The gene for acidic
CC fibroblast growth factor is located on human chromosome 5. The method of
CC the invention comprises employing a plasmid having at least one copy of
CC gene, which encodes a biologically active hAFGF protein operably linked
CC to a promoter, to transform Escherichia coli. The method is useful for
CC producing recombinant or biologically active hAFGF protein, which is
CC useful in promoting angiogenesis. The present sequence represents a cDNA
CC encoding the human acidic fibroblast growth factor 155 protein (hAFGF155)
CC used in the method of the invention. This sequence has been chemically
CC synthesised using the codons which are most often used by E. coli, to
CC facilitate its expression
XX Sequence 630 BP; 191 A; 152 C; 147 G; 140 T; 0 U; 0 Other;
SQ Query Match 85.1%; Score 536; DB 6; Length 630;
Best Local Similarity 93.3%; Pred. No. 4.3e-134;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB 1 GCCTAGAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
QY 61 GAGCGGATTAACAAATTCCTCTAGAAATAATTTGTTTAACTTAAAGAGGAGATATACA 120
DB 61 GAGCGGATTAACAAATTCCTCTAGAAATAATTTGTTTAACTTAAAGAGGAGATATACA 120
QY 121 TATG-----TTTAACTTCGCCC 138
DB 121 TATGGCTGAAGGGGAAATACACCTTTACAGGTTTAAACGGAAATTTAACTTCGCCC 180
QY 139 CGGGAATTACAAAAAACCCAAAGCTTCTTTACTCAGTAACGGAGGACATTCCTCGCAAT 198
DB 181 CGGGAATTACAAAAAACCCAAAGCTTCTTTACTCAGTAACGGAGGACATTCCTCGCAAT 240
QY 199 TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCGACCGACACATTCAGCTGCA 258
DB 241 TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCGACCGACACATTCAGCTGCA 300
QY 259 ACTCTCGCGCGAAAGCGTTGGAGAGGCTATATCAAGTCACCGAGACTGCGCCAGTACCT 318
DB 301 ACTCTCGCGCGAAAGCGTTGGAGAGGCTATATCAAGTCACCGAGACTGCGCCAGTACCT 360
QY 319 TGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACCCCTAAACGAAATTCCTTGT 378
DB 361 TGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACCCCTAAACGAAATTCCTTGT 420
QY 379 TCTAGAAAAGACTAGAGAAAACCAATTACACAGCTACATATCGAAAAACATGACAGAA 438
DB 421 TCTAGAAAAGACTAGAGAAAACCAATTACACAGCTACATATCGAAAAACATGACAGAA 480
QY 439 GAAGTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAAGCGTGACACCGACTCACTA 498
DB 481 GAAGTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAAGCGTGACACCGACTCACTA 540
QY 499 TGGCCAAAAGGCTATCTTGTCTCGCCACTACCACTGAGCTCCGACTAAGGATCCGAAT 558
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Db      541  TGGCCAAAAGGCTATCTTGTCTGCGCACTACCGAGTCCGAGTCCGAGTAAGGATCCGAATT 600
QY      559  CGAGCTCCGTCGACAAAGCTTGGCGCGCGCAC 588
Db      601  CGAGCTCCGTCGACAAAGCTTGGCGCGCGCAC 630

RESULT 9
ID      AAK98917
XX      AC
XX      AAK98917;
DT      24-MAY-2002 (first entry)
XX      Codon optimised synthetic human acidic fibroblast growth factor (155AA).
DE      Human acidic fibroblast growth factor; phage T7 polymerase promoter;
KW      lysis, phase dependent superproduction; synthetic; codon optimisation;
KW      gene; ds.
XX      Homo sapiens.
OS      Synthetic.
FH      Key
CDS     122..589
        /tag= a
        /product= "Protein of human acidic fibroblast growth
        factor (155AA)"
XX      WO200214468-A2.
XX      21-FEB-2002.
XX      15-AUG-2001; 2001WO-US025477.
XX      15-AUG-2000; 2000US-0225437P.
XX      (PHAG-) PHAGE BIOTECHNOLOGY CORP.
XX      Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX      WPI; 2002-269184/31.
DR      P-PSDB; AAO19990.
XX      Bacteriophage-dependent method for producing biologically active proteins
XX      or peptides, involves employing an Escherichia coli transformed with a
XX      plasmid containing the targeted gene(s) operably linked to a promoter.
PS      Claim 23; Fig 1; 44pp; English.
XX      The invention relates to a method for enhancing the production of a
XX      biologically active protein comprising infecting a strain of Escherichia
XX      coli, which has been transformed with a plasmid having at least one copy
XX      of an expressible gene, such as a human acidic fibroblast growth factor.
XX      The expressible gene encodes a biologically active protein operably
XX      linked to a phage T7 polymerase promoter, with a bacteriophage capable of
XX      mediating delayed lysis. The method is useful for the phase dependent
XX      superproduction of biologically active protein and peptides. The method
XX      is particularly useful for enhancing the production of heterologous
XX      proteins in bacterial host cells. This polynucleotide sequence represents
XX      codon optimised DNA of a synthetic human acidic growth factor (155AA) of
XX      the invention. This sequence is an alternative coding sequence for SEQ ID
XX      2 (AAO19990)
SQ      Sequence 630 BP; 191 A; 152 C; 147 G; 140 T; 0 U; 0 Other;
Query Match      85.1%; Score 536; DB 6; Length 630;
Best Local Similarity 93.3%; Pred. No. 4.3e-134;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY      1  GCGTAGAGGATCGAGATCTCGATCCGCGAAATTAATACGACTCCTATAGGGGAATTGT 60
```

```
Db      1  GCGTAGAGGATCGAGATCTCGATCCGCGAAATTAATACGACTCCTATAGGGGAATTGT 60
QY      61  GAGCGGATAACAATTCCTCTAGAAAATAATTTGTTAACTTTAAGAGGAGATATACA 120
Db      61  GAGCGGATAACAATTCCTCTAGAAAATAATTTGTTAACTTTAAGAGGAGATATACA 120
QY      121  TATG-----TTTAACTTCCGCC 138
Db      121  TATGGCTGAAGGGGAAATCACCACCTTTACAGCGTTAACGGGAGAAATTTAACTTCCGCC 180
QY      139  CGGGAATTACAAAAACCCRAAGCTTCTTTACTGCAGTAACGGAGGACACTTCTCTCGCAAT 198
Db      181  CGGGAATTACAAAAACCCRAAGCTTCTTTACTGCAGTAACGGAGGACACTTCTCTCGCAAT 240
QY      199  TCTGCAGATGGCAGTAGATGGGACTCGCGATCGCTCCGACCAGACACATTTCAGCTGCA 258
Db      241  TCTGCAGATGGCAGTAGATGGGACTCGCGATCGCTCCGACCAGACACATTTCAGCTGCA 300
QY      259  ACTCTCGGCCAAAAGCGTTGGAGAGGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 318
Db      301  ACTCTCGGCCAAAAGCGTTGGAGAGGTCTATATCAAGTCGACGGAGACTGGCCAGTACCT 360
QY      319  TGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCTAACGAAGAATGCTTGTT 378
Db      361  TGCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGCTAACGAAGAATGCTTGTT 420
QY      379  TCTAGAAAGACTAGAAAACCATTTACAAACACATACATATCGAAAAAACATGCAGAGAA 438
Db      421  TCTAGAAAGACTAGAAAACCATTTACAAACACATACATATCGAAAAAACATGCAGAGAA 480
QY      439  GAACGTGTTGTAGGCTTAAAAAATGGTTCCTGTAAGCGTGGACACACGAGCTCATA 498
Db      481  GAACGTGTTGTAGGCTTAAAAAATGGTTCCTGTAAGCGTGGACACACGAGCTCATA 540
QY      499  TGGCCAAAAGGCTATCTTGTTCCTGCGCACTACCGAGTCCGAGTCCGAGTCCGAATT 558
Db      541  TGGCCAAAAGGCTATCTTGTTCCTGCGCACTACCGAGTCCGAGTCCGAGTCCGAATT 600
QY      559  CGAGCTCCGTCGACAAAGCTTGGCGCGCGCAC 588
Db      601  CGAGCTCCGTCGACAAAGCTTGGCGCGCGCAC 630

RESULT 10
AD055200
ID      AD055200 standard; DNA; 630 BP.
XX      AC
XX      AD055200;
DT      09-SEP-2004 (first entry)
XX      Human acidic fibroblast growth factor (haFGF) DNA seqid 1.
XX      neangiogenesis stimulator; cardiant; vasotropic; revascularisation;
XX      ischaemic region; fibroblast growth factor-1; FGF-1; neangiogenesis;
XX      acidic FGF; arGF; bacteriophage lambda; coronary artery disease;
XX      myocardial perfusion; revascularisation therapy; ischaemic myocardium;
XX      human; gene; ds.
OS      Homo sapiens.
OS      Synthetic.
XX      Key
CDS     122..589
        /tag= a
        /product= "haFGF"
        /note= "human acidic fibroblast growth factor"
XX      FT
XX      125..589
        /tag= b
        /product= "processed haFGF"
        /note= "human acidic fibroblast growth factor"
XX      FT
XX      /partial
```


PT from plasmid RP4.
 PS Claim 11; Page 14-19; 35pp; French.
 XX This is the nucleotide sequence of a novel expression plasmid derived
 CC from the pT series of expression vectors. The plasmid retains the T7
 CC phage gene 10 promoter and transcriptional terminator for expression of
 CC heterologous proteins e.g. basic fibroblast growth factor. The novelty of
 CC the plasmid derives from the inclusion of the plasmid stability region of
 CC plasmid RP4. This region allows maintenance of the plasmid and prevents
 CC plasmid loss without the need for antibiotic resistance genes for
 CC selection and maintenance. The RP4 par region comprises the genes para,
 CC B, C, D and E. They are placed in the plasmid under control of the lacO
 CC operator and lacI(q) repressor. The novel plasmid can be used to express
 CC proteins of pharmaceutical, agricultural or biocatalytic interest without
 CC the use of antibiotics in the culture medium which, when present in trace
 CC amounts in final preparations, could lead to undesired side effects or
 CC antibiotic resistant microorganisms flourishing
 XX
 SQ Sequence 8501 BP; 1862 A; 2422 C; 2426 G; 1791 T; 0 U; 0 Other;

Query Match 54.2%; Score 341.6; DB 2; Length 8501;
 Best Local Similarity 77.3%; Pred. No. 2.1e-81;
 Matches 447; Conservative 0; Mismatches 89; Indels 42; Gaps 1;

QY 15 GATCTCGATCCCGGAAATTAATACGACTCATTATAGGGGAATTGTGACGGATTAACAAAT 74
 DB 1 GATCTCGATCCCGGAAATTAATACGACTCATTATAGGGGAATTGTGACGGATTAACAAAT 60
 QY 75 TCCCTCTAGAAATTAATTTGTTTAACTTTAAGAGGAGATATACATAT----- 123
 DB 61 TCCCTCTAGAAATTAATTTGTTTAACTTTAAGAGGAGATATACATATGGCTGAGGGG 120
 QY 124 -----GTTTAACTTCCCGCCGGGAATTACAAA 152
 DB 121 AAATCACCACCTTACAGCCCTGACCGAAGTGTAACTGCTCCAGGGAATTACAGA 180
 QY 153 AACCCAGCTTCTTACTGAGTAACGAGGAGACACTTCTCGGAATTCGCCAGATGGCA 212
 DB 181 AGCCCAAACTCTCTACTAGCAACGGGGCCACTTCTGAGGATCTCTCCGGATGGCA 240
 QY 213 CAGTAGATGGGACTCGGATCGCTCCGACACGACATTCAGCTGCAATCTCGGCCGAAA 272
 DB 241 CAGTGTATGGGACAAAGGACAGAGGACAGCACATTCAGCTGCACTCAGTCGGGAAA 300
 QY 273 GCGTTGGAGAGGTCTATATCAAGTCSAGGAGACTGGCCAGTACCTTGCCATGGACACCG 332
 DB 301 GCGTGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCG 360
 QY 333 ATGGGCTTCTGTATGGCTCAGACAGCCCTAACGAAGATGCTTGTCTAGAAAGACTAG 392
 DB 361 ACGGGCTTTTATACGGCTCAGACACCAACCAATGAGGAATGTTTGTCTGGAAAGGCTGG 420
 QY 393 AAGAAAAACATTTACACAGTATCATATCGAAAAAATCATGACGAGAACTCGTTTGTAG 452
 DB 421 AGAGAACCTTTACAAACCTATATATCCAGAGCATGACGAGAGAAATTTGTTTGTG 480
 QY 453 GCCTTAAAAAATGTTTCTGTAAGCGTGGACCGGACTCAGTATGCGCCAAAAGGCTTA 512
 DB 481 GCCTCAAGAAGAAATGGGAGCTCGAAACGGGCTCTCGGACTCAGTATGCGCAGAAAGCA 540
 QY 513 TCTTGTCTCGGACTACGAGTGGCTCGGACTAGGA 550
 DB 541 TCTTGTCTCTCCCTGCGGCTCTCTCTCTGATTAAGA 578

RESULT 12
 ID AAQ02421 standard; cDNA; 454 BP.
 XX
 AC AAQ02421;
 XX
 DT 25-MAR-2003 (revised)

DT 06-AUG-1990 (first entry)
 XX cDNA encoding human acidic fibroblast growth factor.
 DE
 XX Gastro-intestinal ulcer; ileitis; colitis; angiogenesis; ss.
 KW
 XX Synthetic.
 OS
 XX WO9001941-A.
 PN
 XX 08-MAR-1990.
 PD
 XX 11-AUG-1989; 89WO-US003467.
 PF
 XX 19-AUG-1988; 88US-00234966.
 PR
 XX 20-JUL-1989; 89US-00382263.
 PP
 XX (CHIL-) CHILDRENS MED CENT.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Folkman MJ, Kato K;
 PI
 XX WPI; 1990-099254/13.
 DR
 XX Acid-resistant fibroblast growth factor compsns. - used to treat
 PT ulcerative diseases of the gastrointestinal tract in mammals.
 PT
 XX Example 4; Fig 1; 42pp; English.
 PS
 XX This cDNA as inserted into pUC18 to yield pTB917 which was cleaved and
 CC ligated into pEF3c to construct pTB975. This vector was used to transform
 CC E. coli MM294 (DE3)/plys. Transforms were cultured to produce human
 CC acidic FGF which can be used in compsns. for treating ulcerating diseases
 CC of the GI tract. (Updated on 25-MAR-2003 to correct PA field.)
 CC
 SQ Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;

Query Match 46.0%; Score 290; DB 2; Length 454;
 Best Local Similarity 80.0%; Pred. No. 6.7e-68;
 Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 122 ATGTTTAACTTCCCGCCGGGAATTACAAAAAACCAGCTTCTTTACTGCAGTAACGGA 181
 DB 14 ATGTTTAACTTCCCGCCGGGAATTACAAAGGCCCAACTCTCTACTGCAGCAACGGG 73
 QY 182 GGACACTTCTCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCCGAC 241
 DB 74 GGCCACTTCTCGAGGATTCCTCCGATGGCACAGTGGATGGGACAAGGGACAGGAGCGAC 133
 QY 242 CAGCACATTAGCTGCAACTCTCGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGACG 301
 DB 134 CAGCACATTAGCTGCAACTCAGTGCAGAAACGCTGGGGAGGTTATATAAAGAGTACC 193
 QY 302 GAGACTGCCAGTAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCAGACAGCGCT 361
 DB 194 GAGACTGCCAGTAGTACTTGGCAATGGACACCGACGGGCTTTATAGGCTCAGACACCA 253
 QY 362 AACGAAGAATGTTGTTTCTAGAAAGACTAGAAAGAAACCAATTACAAACGCTACATATCG 421
 DB 254 AATGAGGAATGTTGTTTCTTGGAAAGCTGGAGGAGAAACCAATTACAAACCTATATATCC 313
 QY 422 AAAAAACATGACAGAGAACTGTTTGTAGGCCCTTAAAAAATGTTCTCTGTAAGCGT 481
 DB 314 AAGAAGCATGACAGAGAAAGATTTGTTTGTGGCCCTCAAGAAGATGGGAGCTGCAACGC 373
 QY 482 GGACACGGACTCAGTATGGCCAAAAGGCTATCTTGTTCCTGCCACTACCAAGTACGCTCC 541
 DB 374 GGTCTCGGACTCAGTATGGCCAAAGGCAATCTTGTTCCTCCCTGCCAGTCTCTCTCT 433
 QY 542 GACTAA 547
 DB 434 GATTAA 439

Db	374	GGTCCTCGGACTCACTATGCGCAGAAAGCAATCTTGTGTTTCTCCCCCTCCAGTCTCTTCT	433
Qy	542	GAATAA 547	
Db	434	GATTAA 439	
RESULT 14			
AAQ10399			
ID	AAQ10399	standard; cDNA; 454 BP.	
XX	AAQ10399;		
AC	25-MAR-2003	(revised)	
DT	15-APR-1991	(first entry)	
DE	Human acidic fibroblast growth factor gene.		
XX	aFGF; antibody; antigen; cancer; ss.		
OS	Homo sapiens.		
Key	Location/Qualifiers		
FT	14..442		
FT	/*tag= a		
FT	/product= "aFGF"		
XX	JP02306996-A.		
XX	20-DEC-1990.		
XX	03-JUL-1989;	89JP-00172542.	
XX	04-JUL-1988;	88JP-00166275.	
XX	(TAKE) TAKEDA CHEM IND LTD.		
XX	WPI; 1991-040150/06.		
XX	P-PSDB; AAR10527.		
XX	Anti-acid antibody, for cancer diagnosis, etc. - is obtd. by using		
XX	complex of partial peptide(s) of acid fibroblast growth factor and		
XX	protein as antigen.		
XX	Disclosure; Fig 1; 19pp; Japanese.		
XX	The sequence can be used to produce recombinant aFGF in plasmid pTB975.		
XX	Peptides derived from the protein can be used to as antigens to produce		
XX	anti-aFGF antibodies. The Abs can be used for immunochemically measuring		
XX	aFGF, and for purifying aFGF. They are useful as reagents in the		
XX	diagnosis of various cancers or diseases of the CNS. Purified aFGF has		
XX	wound healing and nerve cell proliferating properties. (Updated on 25-MAR		
XX	-2003 to correct PA field.)		
XX	Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;		
Query Match 46.0%; Score 290; DB 2; Length 454;			
Best Local Similarity 80.0%; Pred. No. 6.7e-68;			
Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;			
Qy	122	ATGTTTAACTTCGCGCCGGGAATTACAAAAACCCAAAGCTTCTTTACTGCACTAAGCGG 181	
Db	14	ATGTTTAACTTCGCGCCGGGAATTACAAAAACCCAAAGCTTCTTTACTGCACTAAGCGG 73	
Qy	182	GGACACTTCCTGCGAATTCCTCGCGGAAAGCGTTGGAGAGGTCCTATATCAATCG 241	
Db	74	GGCCACTTCCTGAGATTCTCCGGATGGCAGTGGGACAGGAGCGGAC 133	
Qy	242	CAGCAGATTGAGTGGCACTCTCGCGGAAAGCGTTGGAGAGGTCCTATATCAATCG 301	
Db	134	CAGCAGATTGAGTGGCACTCTCGCGGAAAGCGTTGGAGAGGTCCTATATCAATCG 193	
Qy	302	GAGACTGGCCAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACG 361	
Db	194	GAGACTGGCCAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACG 253	
Qy	362	AACGAAGATGCTGCTTCTAGAAAGACTAGAAACCAATTAACACACGATCATATCG 421	
Db	254	AATGAGGATGTTTCTGGAAGGCTGGAGAGCACTTACACACCTATATATCC 313	
Qy	422	AAAAACATGAGAGAGGAGTGGTTTCTAGCGCTTAAAAAAATGGTTCCTGTAAGCGT 481	
Db	314	AAGAGCATGAGAGAGGAGTGGTTTCTAGCGCTTAAAAAAATGGTTCCTGTAAGCGT 373	
Qy	482	GGACACCGGACTACTATGGCCAAAGGCTATCTGTGCTGCCACTACCACTGAGCTCC 541	

Db 194 GAGACTGGCCAGTACTTGGCAATGGACACCGAGGGCTTTATAGGGCTCAGACACCA 253
 QY 362 AACGAAGATGCTGTTCTTAGAAGACTAGAGAAACCATTTACAAACGTAATATCG 421
 Db 254 AATGAGGATGTTGTTCTGGAAGGCTGGAGGAGCAATTAACAACCTATATATCC 313
 QY 422 AAAAAACATGCAGAGAGAACTGGTTTGTAGGCCTTAAAAAATGGTTCTGTAAAGCT 481
 Db 314 AAGAAGCATGCAGAGAAAGATTTGGTTTGGCCCTCAAGAAGATGGGAGCTGCAACGC 373
 QY 482 GGACACGAGCTCACTATATGCCAAAGGCTATCTTGTCTCCACTACCACTGAGCTCC 541
 Db 374 GGTCTCGGACTCACTATATGCCAAAGCAATCTTGTCTCCCTGCCAGTCTCTTCT 433
 QY 542 GACTAA 547
 Db 434 GATTAA 439

RESULT 15

AAQ10166
 ID AAQ10166 standard; cDNA; 454 BP.

XX AC AAQ10166;

XX 25-MAR-2003 (revised)

DT 19-MAR-1991 (first entry)

XX Human acidic fibroblast growth factor encoding sequence.

DE aFGF; wound healing; pTB917; ds.

XX Homo sapiens.

XX Key

FT CDS

FT 14..435

FT /*tag= a

XX EP406738-A.

XX 09-JAN-1991.

XX 30-JUN-1990; 90EP-00112532.

XX 03-JUL-1989; 89JP-00172542.

XX 29-SEP-1989; 89JP-00256193.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1991-009738/02.

XX Production of acidic FGF protein - using expression vector to transform

PT host cells and express aFGF gene.

XX Disclosure; Fig 1; 23pp; English.

XX Sequence may be used to transform an E.coli expression system, allowing

CC for efficient production of the aFGF, useful in promotion of wound

CC healing. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 454 BP; 127 A; 110 C; 119 G; 98 T; 0 U; 0 Other;

Query Match 46.0%; Score 290; DB 2; Length 454;

Best Local Similarity 80.0%; Pred. No. 6.7e-68;

Matches 341; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 122 ATGTTTAACCTTCCGCCCGGGAATTACAAAACCCAGCTTCTTACTGCGAGTAACGGA 181

Db 14 ATGTTTAATCTCGCTCCCGGGAATTACAAAGAGCCCAACTCTCTACTGCAACCGG 73

QY 182 GGACACTTCTCGGAATTTCTGCAGATGGCAGTAGATGGGACTCGCGATCGCTCCGAC 241

Db 74 GGCCACTTCCCTGAGGATTTCTCCGATGGCACAGTGGATGGGACAAAGGACAGGACGAC 133
 QY 242 CAGCACATTTACGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGCTTATATCAAGTCCGACG 301
 Db 134 CAGCACATTTACGCTGCAACTCAGTCCGGAAGCGTTGGGGAGGTTATATAAAGAGTACC 193
 QY 302 GAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCT 361
 Db 194 GAGACTGGCCAGTACTTTGGCAATGGACACCGGCTTTTATACGGCTCACAGACCA 253
 QY 362 AACGAAGATGCTTGTGTTCTAGAAAGACTAGAAAGAAACCATTTACAAACGTAATATCG 421
 Db 254 AATGAGGATGTTGTTCTCGGAAGGCTGGAGGAGCAATTTACAAACCTATATATCC 313
 QY 422 AAAAAACATGCAGAGAGAACTGGTTTGTAGGCCTTAAAAAATGGTTCTGTAAAGCT 481
 Db 314 AAGAAGCATGCAGAGAAAGATTTGGTTTGGCCCTCAAGAAGATGGGAGCTGCAACGC 373
 QY 482 GGACACGAGCTCACTATATGCCAAAGGCTATCTTGTCTCCACTACCACTGAGCTCC 541
 Db 374 GGTCTCGGACTCACTATATGGCCAGAAAGCAATCTTGTCTCCCTGCCAGTCTCTTCT 433
 QY 542 GACTAA 547
 Db 434 GATTAA 439

Search completed: June 17, 2005, 00:49:05
 Job time : 480 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 00:27:22 ; Search time 164 Seconds
(without alignments)
6285.697 Million cell updates/sec

Title: US-10-649-480A-6
Perfect score: 630
Sequence: 1 gcgtagagatcgagatctc.....ctgagatcggtgctaaca 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	630	4	US-09-929-945-6
2	630	100.0	630	4	US-09-929-918-6
3	584	92.7	630	4	US-09-929-945-4
4	584	92.7	630	4	US-09-929-918-4
5	567.4	90.1	990	4	US-09-929-918-10
6	536	85.1	630	4	US-09-929-945-1
7	536	85.1	630	4	US-09-929-918-1
8	341.6	54.2	8501	3	US-08-793-900-1
9	290	46.0	454	6	5175147-1
10	290	46.0	454	6	5175147-1
11	285.4	45.3	490	4	US-09-023-655-1390
12	285.4	45.3	638	3	US-09-098-628-3
13	284	45.1	468	4	US-09-929-945-3
14	284	45.1	468	4	US-09-929-918-3
15	242	38.4	450	6	5437995-1
16	242	38.4	450	6	5437995-1
17	221.8	35.2	454	3	US-09-030-613-14
18	221.8	35.2	454	3	US-09-451-905-14
19	141.6	22.5	261	1	US-08-070-165F-1
20	141.6	22.5	261	2	US-08-885-418-1
21	141.6	22.5	477	1	US-08-230-373B-16
22	131.4	20.9	483	3	US-09-220-077C-1
23	131.4	20.9	483	4	US-09-826-210A-1
24	131.4	20.9	483	4	US-09-722-495A-1
25	128	20.3	442	3	US-09-385-114-1
26	128	20.3	442	3	US-09-417-721-4
27	125.6	19.9	5443	2	US-08-929-967-1

c	28	125.2	19.9	6361	3	US-08-646-538-7	Sequence 7, Appli
c	29	125.2	19.9	6361	3	US-09-503-222-7	Sequence 7, Appli
	30	124.4	19.7	3572	3	US-09-072-596-337	Sequence 337, App
	31	124.4	19.7	3572	3	US-09-072-967-342	Sequence 342, App
	32	124.4	19.7	7676	3	US-09-056-556-213	Sequence 213, App
	33	124.4	19.7	7676	3	US-09-072-596-208	Sequence 208, App
	34	124.4	19.7	7676	4	US-09-072-967-213	Sequence 213, App
	35	124.4	19.7	7676	4	US-09-287-849-9	Sequence 9, Appli
	36	124	19.7	1010	3	US-09-070-408-1	Sequence 1, Appli
	37	124	19.7	5502	4	US-09-702-705-785	Sequence 785, App
	38	124	19.7	5502	4	US-09-736-457-785	Sequence 785, App
	39	124	19.7	5502	4	US-09-614-124B-785	Sequence 785, App
	40	124	19.7	5502	4	US-09-671-325-785	Sequence 785, App
	41	124	19.7	5502	4	US-09-589-184-785	Sequence 785, App
	42	124	19.7	5502	4	US-09-658-824-785	Sequence 785, App
	43	124	19.7	6353	4	US-09-702-705-784	Sequence 784, App
	44	124	19.7	6353	4	US-09-736-457-784	Sequence 784, App
	45	124	19.7	6353	4	US-09-614-124B-784	Sequence 784, App

ALIGNMENTS

RESULT 1
US-09-929-945-6
; Sequence 6, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (140 amino acids) using
; OTHER INFORMATION: preferred codons for E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(544)
US-09-929-945-6

Qy	1	GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATACGACTCCTATAGGGGAATGT	60
Db	1	GCCTAGAGATCGAGATCTCGATCCCGCGAAATTAATACGACTCCTATAGGGGAATGT	60
Qy	61	GAGCGGATACAAATCCCTCTAGAAATATTTTGTAACTTTAAGAGAGATATACA	120
Db	61	GAGCGGATACAAATCCCTCTAGAAATATTTTGTAACTTTAAGAGAGATATACA	120
Qy	121	TATGTTTAACTTTCCGCCCGGGAATTAACAAAAACCAAGCTTTTCTTCTGAGTAACGG	180
Db	121	TATGTTTAACTTTCCGCCCGGGAATTAACAAAAACCAAGCTTTTCTTCTGAGTAACGG	180
Qy	181	AGGACACTTCTCGGAATTCGCGAGATGCGACAGTAGTGGGACTCGCGATCCTCCGA	240
Db	181	AGGACACTTCTCGGAATTCGCGAGATGCGACAGTAGTGGGACTCGCGATCCTCCGA	240
Qy	241	CCAGCACATTGAGTCTCTCGCGGCGAAAGCTTTGGAGAGGCTCTATATCAAGTCGAC	300

241	Db	 CCAGCACATTCAAGCTCGCAACTCTCGCGCGAAAGCGTTTGGAGAGGCTCTATATCAAGTCGAC	300
301	Qy	 GGAGACTGCGCCAGTAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCAGACAGCGC	360
301	Db	 GGAGACTGCGCCAGTAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCAGACAGCGC	360
361	Qy	 TAAACGAAGAATCGTTGTGTTTCTATGAAGACTAGAGAAGAAACCATTTACAAACGTCACATATC	420
361	Db	 TAAACGAAGAATCGTTGTGTTTCTATGAAGACTAGAGAAGAAACCATTTACAAACGTCACATATC	420
421	Qy	 GAAAAACAATGCAGAGAAGAACTGGTTTGTAGGCGCTTAAAAAAATGGTTCTGTAAAGCG	480
421	Db	 GAAAAACAATGCAGAGAAGAACTGGTTTGTAGGCGCTTAAAAAAATGGTTCTGTAAAGCG	480
481	Qy	 TGGACCACCGACTCACTATGGCCAAAAGGCTATCTTGTTCCTGCGCATACCACTGAGCTC	540
481	Db	 TGGACCACCGACTCACTATGGCCAAAAGGCTATCTTGTTCCTGCGCATACCACTGAGCTC	540
541	Qy	 CGACTTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGCGGCACTCGACGACCAACC	600
541	Db	 CGACTTAAGGATCCGAATTCGAGCTCCGTCGACAAAGCTTGGCGCGGCACTCGACGACCAACC	600
601	Qy	 ACCACCACCACTGAGATCCGGCTGCTAAACA	630
601	Db	 ACCACCACCACTGAGATCCGGCTGCTAAACA	630

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RESULT 2
US-09-929-918-6
; Sequence 6, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozitanov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1993-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a chemically synthesized sequence
; OTHER INFORMATION: encoding a 140 amino acid form of fibroblast
; OTHER INFORMATION: growth factor with alterations for preferred codon
; OTHER INFORMATION: usage in E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(544)
; US-09-929-918-6

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Db	121	TATGTTTAACTTCCGCCCGGGAAATTACAAAAAACCACAAAGCTTCTTTTACTCGAGTAAACGG	180
Qy	181	AGGACACTTCTCTCGGAATTTCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	240
Db	181	AGGACACTTCTCTCGGAATTTCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGA	240
Qy	241	CCAGCAATTTCAGTGTCAACTCTCTCGGCCGAAAGGTTGGAGAGGTCTATATCAAGTCGAC	300
Db	241	CCAGCAATTTCAGTGTCAACTCTCTCGGCCGAAAGGTTGGAGAGGTCTATATCAAGTCGAC	300
Qy	301	GGAGACTGGCCAGTACCTTGGCATGGACACCCGATGGGCTTCTGTATGGCTCACAGACGCC	360
Db	301	GGAGACTGGCCAGTACCTTGGCATGGACACCCGATGGGCTTCTGTATGGCTCACAGACGCC	360
Qy	361	TACGAAGAATGCTGTGTTTCTAGAAAGACTAGAGAAAGAAACCAATTACACAGTACATATC	420
Db	361	TACGAAGAATGCTGTGTTTCTAGAAAGACTAGAGAAAGAAACCAATTACACAGTACATATC	420
Qy	421	GAAAAAACAATGCAGAGAAAGAACTGGTTTGATAGGCTTAAAAAAAATGGTTCTGTGAAGCG	480
Db	421	GAAAAAACAATGCAGAGAAAGAACTGGTTTGATAGGCTTAAAAAAAATGGTTCTGTGAAGCG	480
Qy	481	TGGACCAACGAGACTCACTATATGGCCAAAAAGGCTATCTTGTTCTGGCACTACCAAGTGAAGTC	540
Db	481	TGGACCAACGAGACTCACTATATGGCCAAAAAGGCTATCTTGTTCTGGCACTACCAAGTGAAGTC	540
Qy	541	CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGCCGCACTCCGAGCACCAACC	600
Db	541	CGACTAAGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGCCGCACTCCGAGCACCAACC	600
Qy	601	ACCACCAACCACTGAGATCCCGCTGCTAACCA	630
Db	601	ACCACCAACCACTGAGATCCCGCTGCTAACCA	630

```

RESULT 3
US-09-929-945-4
; Sequence 4, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (134 amino acids) using
; OTHER INFORMATION: preferred codons for E. coli
; NAME/KEY: CDS
; LOCATION: (122)...(526)
; US-09-929-945-4

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	Query Match	92.7%	Score 584;	DB 4;	Length 630;
	Best Local Similarity	97.1%;	Pred. No. 1.5e-169;		
	Matches 612; Conservative	0;	Mismatches	0;	Indels 18; Gaps 1
Qy		1	GCGTAGAGGATCGAGATCTCGATCCCGCAAATTAAATACGACTCACTATAGGGGAATTGT		60
Dd		1	GCGTAGAGGATCGAGATCTCGATCCCGCAAATTAAATACGACTCACTATAGGGGAATTGT		60
Ov		61	GAGCGGATAACAATTTCCTCTTAGAAAATAATTTTGTTTAACCTTTAAGAAGAGAGATATACA		120

; LOCATION: (231)...(249)
; NAME/KEY: CDS
; LOCATION: (320)...(784)
US-09-929-918-10

Query Match 90.1%; Score 567.4; DB 4; Length 990;
Best Local Similarity 92.8%; Pred. No. 2.4e-164;
Matches 623; Conservative 0; Mismatches 6; Indels 42; Gaps 1;

QY	2	CGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTACATATAGGGGAATTGTG	61
Db	200	CGTGGGGCGCGAGATCTCGATCCCGGAAATTAATACGACTACATATAGGGGAATTGTG	259
QY	62	ACGGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGATATACAT	121
Db	260	ACGGGATACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGATATACAT	319
QY	122	ATG-----TTTAACTTCCGCC	139
Db	320	ATGGCTGAAGGGGAATACACCCTTTACAGCGTTAACGGAGAAATTTAACCTTCCGCC	379
QY	140	GGGAATTAACAAAAACCAAGCTTCTTTACTGAGTAACGGAGGACATTTCTGCGAATT	199
Db	380	GGGAATTAACAAAAACCAAGCTTCTTTACTGAGTAACGGAGGACATTTCTGCGAATT	439
QY	200	CTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA	259
Db	440	CTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA	499
QY	260	CTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCTT	319
Db	500	CTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCTT	559
QY	320	GCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTTAAACGAAATGCTTGT	379
Db	560	GCATGGACACCGATGGGCTTCTGTATGGCTCACAGACGCTTAAACGAAATGCTTGT	619
QY	380	CTAGAAGACTAGAGAAACCAATACACAGTACATATCGAAAAACATCGAGAG	439
Db	620	CTAGAAGACTAGAGAAACCAATACACAGTACATATCGAAAAACATCGAGAG	679
QY	440	AACTGGTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCGGACTCACTAT	499
Db	680	AACTGGTTGTAGGCTTAAAAAATGTTCTCTGAAGCGTGGACCGGACTCACTAT	739
QY	500	GGCCAAAAGGCTATCTTTCTGCGACTACCAAGTGGCTCCGACTAAGGATCCGAATTC	559
Db	740	GGCCAAAAGGCTATCTTTCTGCGACTACCAAGTGGCTCCGACTAAGGATCCGAATTC	799
QY	560	GAGCTCCGTCGACAGCTTGGGCGCGACTCGAGCACACACGACCACTGAGATCC	619
Db	800	GAGCTCCGTCGACAGCTTGGGCGCGACTCGAGCACACACGACCACTGAGATCC	859
QY	620	GGCTGCTAAC 630	
Db	860	GGCTGCTAAC 870	

RESULT 6
US-09-929-945-1
; Sequence 1, Application US/09929945
; Patent No. 664206
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Olexandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: FIBROBLAST GROWTH FACTOR 155
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using
; NAME/KEY: CDS
; LOCATION: (122)...(590)
US-09-929-945-1

Query Match 85.1%; Score 536; DB 4; Length 630;
Best Local Similarity 93.3%; Pred. No. 9e-155;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY	1	CGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTACATATAGGGGAATTGT	60
Db	1	CGTAGAGGATCGAGATCTCGATCCCGGAAATTAATACGACTACATATAGGGGAATTGT	60
QY	61	GAGCGGATAACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGATATACA	120
Db	61	GAGCGGATAACAAATCCCTCTAGAAATTAATTTGTTAACTTTAAGAGGATATACA	120
QY	121	TATG-----TTTAACTTCCGCC	138
Db	121	TATGCTGAAGGGGAATCACACCTTTTACAGCGTTAACGGAGAAATTTAACCTTCCGCC	180
QY	139	CGGGAATTTACAAAAACCAAGCTTCTTTACTGAGTAACGGAGGACATTTCTGCGAAT	198
Db	181	CGGGAATTTACAAAAACCAAGCTTCTTTACTGAGTAACGGAGGACATTTCTGCGAAT	240
QY	199	TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA	258
Db	241	TCTGCCAGATGGCACAGTAGATGGGACTCGGATCGCTCCGACGACACATTCAGCTGCA	300
QY	259	ACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCT	318
Db	301	ACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGACGAGACTGGCCAGTACCT	360
QY	319	TGCCATGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAAAGAAATGCTTGT	378
Db	361	TGCCATGACACCGATGGCTTCTGTATGGCTCACAGACGCTTAAAGAAATGCTTGT	420
QY	379	TCTAGAAGACTAGAGAAACCAATTAACAACGCTACATATCGAAAAACATCGAGAGAA	438
Db	421	TCTAGAAGACTAGAGAAACCAATTAACAACGCTACATATCGAAAAACATCGAGAGAA	480
QY	439	GAACTGGTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACACCGGACTCACTA	498
Db	481	GAACTGGTTGTAGGCTTAAAAAATGTTCTGTAAAGCGTGGACACCGGACTCACTA	540
QY	499	TGGCCAAAAGGCTATCTTTCTGCGACTACCAAGTGGCTCCGACTAAGGATCCGAAT	558
Db	541	TGGCCAAAAGGCTATCTTTCTGCGACTACCAAGTGGCTCCGACTAAGGATCCGAAT	600
QY	559	CGAGCTCCGTCGACAAAGCTTGGCGCCGCCAC 588	
Db	601	CGAGCTCCGTCGACAAAGCTTGGCGCCGCCAC 630	

RESULT 7
US-09-929-918-1
; Sequence 1, Application US/09929918
; Patent No. 677389
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Olexandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

;; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
;; FILE REFERENCE: PHAGE 006A
;; CURRENT APPLICATION NUMBER: US/09/929,918
;; CURRENT FILING DATE: 2001-08-15
;; PRIOR APPLICATION NUMBER: 09/318,288
;; PRIOR FILING DATE: 1999-05-25
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 630
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: This sequence was chemically synthesized based
;; OTHER INFORMATION: upon the amino acid sequence of human acidic
;; OTHER INFORMATION: fibroblast growth factor (155 amino acids) using
;; OTHER INFORMATION: codons which are used in highly expressed proteins from E. coli.
;; NAME/KEY: CDS
;; LOCATION: (122)...(590)
;; US-09-929-918-1

Query Match 85.1%; Score 536; DB 4; Length 630;
Best Local Similarity 93.3%; Pred. No. 9e-155;
Matches 588; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 1 GCCTAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||
QY 1 GCCTAGGATCGAGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGT 60
DB |||||
QY 61 GACGGATACAAATTCCTCTAGAAATATTTTGTAACTTTAAGAAGGAGATATACA 120
DB |||||
QY 61 GACGGATACAAATTCCTCTAGAAATATTTTGTAACTTTAAGAAGGAGATATACA 120
DB |||||
QY 121 TATG-----TTTAACTTCGGCC 138
DB |||||
QY 121 TATGGCTGAAGCGGAATACCACTTTACAGCGTTTAAACGGAGAAATTTAACTTCGGCC 180
DB |||||
QY 139 CGGGAATTACAAAACCCAGCTTCTTTACTGCTAGTAACGGAGGACACTTCTCGGAAT 198
DB |||||
QY 181 CGGGAATTACAAAACCCAGCTTCTTTACTGCTAGTAACGGAGGACACTTCTCGGAAT 240
DB |||||
QY 199 TCTGCCAGATGGCAAGTCTGAGAGGTTCTATATCAAGTCCGATCGCTCCGACGACACATTCAGCTGCA 258
DB |||||
QY 241 TCTGCCAGATGGCAAGTCTGAGAGGTTCTATATCAAGTCCGATCGCTCCGACGACACATTCAGCTGCA 300
DB |||||
QY 259 ACTCTCGCCGAAAGCTTGGAGAGTCTATATCAAGTCCGATCGCTCCGACGACACTGGCCAGTACCT 318
DB |||||
QY 301 ACTCTCGCCGAAAGCTTGGAGAGTCTATATCAAGTCCGATCGCTCCGACGACACTGGCCAGTACCT 360
DB |||||
QY 319 TGCATCGACACCGATGGCTTCTGTATGGCTCAAGACGCTTAAACGAAGTCTGTGT 378
DB |||||
QY 361 TGCATCGACACCGATGGCTTCTGTATGGCTCAAGACGCTTAAACGAAGTCTGTGT 420
DB |||||
QY 379 TCTAGAAGACTAGAAGAAACCAATTAACAACGTCATATCGAAAAACATGCAGAGAA 438
DB |||||
QY 421 TCTAGAAGACTAGAAGAAACCAATTAACAACGTCATATCGAAAAACATGCAGAGAA 480
DB |||||
QY 439 GAATCGTTTGTAGGCTTAAAAAATGTTCTGTAAAGGTGGAACCGACTCACTA 498
DB |||||
QY 481 GAATCGTTTGTAGGCTTAAAAAATGTTCTGTAAAGGTGGAACCGACTCACTA 540
DB |||||
QY 499 TGGCAAAAGCTATCTGTCTCCACTACGATGAGCTCCGACTAAGGATCCGAAT 558
DB |||||
QY 541 TGGCAAAAGCTATCTGTCTCCACTACGATGAGCTCCGACTAAGGATCCGAAT 600
DB |||||
QY 559 CGAGCTCGTGCACAAGCTTCGGCCGAC 588
DB |||||
QY 601 CGAGCTCGTGCACAAGCTTCGGCCGAC 630
DB |||||

RESULT 8
US-08-793-900-1
; Sequence 1, Application US/08793900

;; Patent No. 6143518
;; GENERAL INFORMATION:
;; APPLICANT: CAMERON, Beatrice
;; APPLICANT: CROUZET, Joel
;; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT
;; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Road, Mailstop 3C43
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,900
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/FR95/01178
;; FILING DATE: 14-SEP-1995
;; APPLICATION NUMBER: FR 94/11049
;; FILING DATE: 16-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky Esq., Martin F.
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: ST94069-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 454-3816
;; TELEFAX: (610) 454-3808
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8501 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: cdna
;; US-08-793-900-1

Query Match 54.2%; Score 341.6; DB 3; Length 8501;
Best Local Similarity 77.3%; Pred. No. 2.4e-94;
Matches 447; Conservative 0; Mismatches 89; Indels 42; Gaps 1;

QY 15 GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAAT 74
DB |||||
QY 1 GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAAT 60
DB |||||
QY 75 TCCCTCTAGAAATATTTTGTAACTTTAAGAAGGAGATATACATAT----- 123
DB |||||
QY 61 TCCCTCTAGAAATATTTTGTAACTTTAAGAAGGAGATATACATATCGCTGGAAGGG 120
DB |||||
QY 124 -----GTTTAACTTCGCGCGGAAATTACAAA 152
DB |||||
QY 121 AAATCAACCTTCAAGCCCTGACCGAAGTTTAACTCTCCCTCAGGGAATTTACAGA 180
DB |||||
QY 153 AACCAAGCTTCTTTACTGTCAGTAACCGAGGACAATTCTTCGCAATTTCTCCAGATGCA 212
DB |||||
QY 181 AGCCAACTCTACTGTAGCAACGGGGCCACTTCTCTGAGGATCCTTCCGATGCA 240
DB |||||
QY 213 CAGTATAGGGAATCGCGATCGCTCCGACAGACATTCAGCTGCAACTCTCGGCCGAA 272
DB |||||
QY 241 CAGTATAGGGAATCGCGATCGCTCCGACAGACATTCAGCTGCAACTCTCGGCCGAA 300
DB |||||
QY 273 GCTTGGAGAGTCTATATCAAGTCCAGCGAGACTGCCAGTACCTTGCATGACACCG 332
DB |||||
QY 301 GCGTGGGGAGGTGTATATAAGAGTACCCGAGTCTGGCCAGTACTTGGCCATGACACCG 360
DB |||||
QY 333 ATGGCTTCTGTATGGCTCACAGACGCTTAACGAAGATGCTTGTCTTAGAAAGACTAG 392
DB |||||

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1390:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g396163
US-09-023-655-1390

Query Match 45.3%; Score 285.4; DB 4; Length 490;
Best Local Similarity 78.9%; Pred. No. 1.1e-77;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
Qy 120 ATATGTTTAACTTCCGCGGGAATTACAAAACCCAGCTTCTTACTGCAGTAACG 179
Db 51 AGAAGTTTAACTTCCGCGGGAATTACAAAACCCAGCTTCTTACTGTAGCAACG 110
Qy 180 GAGGACACTTCTCGGGAATTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
Db 111 GGGGCCACTTCTCGGGAATTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 170
Qy 240 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 299
Db 171 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTA 230
Qy 300 CGGAGACTGCCAGTACTTGGCCATGGACACCGGCTTCTGTATGGCTTCACAGACG 359
Db 231 CGGAGACTGCCAGTACTTGGCCATGGACACCGGCTTCTGTATGGCTTCACAGAC 290
Qy 360 CTAAAGGAAGTCTGTTCTAGAAAGACTAGAAAGAAACCAATTACAAACACGTACATAT 419
Db 291 CAATGAGGAATGTTGTTCTGGAAGGCTGGAGGAGACCAATTACAAACCTATATAT 350
Qy 420 CGAAAAACATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGC 479
Db 351 CCAAGAGCATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGC 410
Qy 480 GTGACACCGACTCATTATGGCCAAAGGCTATCTTGTCTCCCTGCCACTACCGAGCT 539
Db 411 GCGGTCTCGGACTCATTATGGCCAAAGGCTATCTTGTCTCCCTGCCACTACCGAGCT 470
Qy 540 CCGACTAAGGA 550
Db 471 CTGATTAAAGA 481

RESULT 12
US-09-098-628-3
Sequence 3, Application US/09098628
Patent No. 6294359
GENERAL INFORMATION:
APPLICANT: FIDDES, J.C.
APPLICANT: ABRAHAM, J.D.
TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
TITLE OF INVENTION: FACTOR ANALOG

NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,628
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 21900-20089.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 91...555
OTHER INFORMATION:
US-09-098-628-3

Query Match 45.3%; Score 285.4; DB 3; Length 638;
Best Local Similarity 78.9%; Pred. No. 1.3e-77;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
Qy 120 ATATGTTTAACTTCCGCGGGAATTACAAAACCCAGCTTCTTACTGCAGTAACG 179
Db 131 AGAAGTTTAACTTCCGCGGGAATTACAAAACCCAGCTTCTTACTGTAGCAACG 190
Qy 180 GAGGACACTTCTCGGGAATTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
Db 191 GGGGCCACTTCTCGGGAATTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 250
Qy 240 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTCGA 299
Db 251 ACCAGCACATTCAGTGCACACTCTCGGCGGAAAGCGTTGGAGAGGCTTATATCAAGTA 310
Qy 300 CGGAGACTGCCAGTACTTGGCCATGGACACCGGCTTCTGTATGGCTTCACAGACG 359
Db 311 CGGAGACTGCCAGTACTTGGCCATGGACACCGGCTTCTGTATGGCTTCACAGAC 370
Qy 360 CTAAAGGAAGTCTGTTCTAGAAAGACTAGAAAGAAACCAATTACAAACACGTACATAT 419
Db 371 CAATGAGGAATGTTGTTCTGGAAGGCTGGAGGAGACCAATTACAAACCTATATAT 430
Qy 420 CGAAAAACATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGC 479
Db 431 CCAAGAGCATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGGTTCTGTAAAGC 490
Qy 480 GTGACACCGACTCATTATGGCCAAAGGCTATCTTGTCTCCCTGCCACTACCGAGCT 539
Db 491 GCGGTCTCGGACTCATTATGGCCAAAGGCTATCTTGTCTCCCTGCCACTACCGAGCT 550

QY 540 CCGACTAAGGA 550
Db 551 CTGATTAAAGA 561

RESULT 13

US-09-929-945-3

; Sequence 3, Application US/09929945
; Patent No. 6642026
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; FILE REFERENCE: FIBROBLAST GROWTH FACTOR 155
; CURRENT APPLICATION NUMBER: US/09/929,945
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-929-945-3

Query Match 45.1%; Score 284; DB 4; Length 468;

Best Local Similarity 79.0%; Pred. No. 3e-77;
Matches 338; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAACCCAAAGTCTCTTACTCGAGTAACG 179

Db 41 AGAAGTTTAACTTCGCGCCGGGAATTACAAAACCCAAAGTCTCTTACTCGAGTAACG 100

QY 180 GAGGACATCTCCGGAATTCGCCAGATGGCACAGTAGATGGGCTCGGATCGCTCGG 239

Db 101 GGGGCCACTTCTCGAGGATCTTCGGATGGCACAGTAGATGGGCAAGGACAGGAGCG 160

QY 240 ACCAGCACATTCAGCTGCAACTCTCGCGCGAAAGCGTTGGAGAGGTCTATATCAAGTCA 299

Db 161 ACCAGCACATTCAGCTGCAACTCAGTGGCGGAAGCGTGGGGAGGTGTATATAAGAGTA 220

QY 300 CGGAGACTGGCGAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG 359

Db 221 CCGAGACTGGCGAGTACCTTGCCATGGACACCGAGCGGCTTTTATACGGCTCACAGACAC 280

QY 360 CTAAAGGAAGTCTGTGTTCTAGAAAGACTAGAGAAACCATTTACAAACGTACATAT 419

Db 281 CAAATGAGGAATGTTGTTCTGGAAGGCTGGAGGAGAACCATTTACAAACCTATATAT 340

QY 420 CGAAAAAATCATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAGC 479

Db 341 CCAAGAGCATGCAGAGAGAAATGTTGTTGGCTCAAGAGAGATGGGAGCTGCAAC 400

QY 480 GTGGACACCGAGTACTATAGGCCAAAGGCTATCTGTCTGCGCACTACCAAGTACGCT 539

Db 401 GCGGTCTCGGACTACTATGGCCAGAAAGCAATCTGTGTTCTCCCGCTGCCAGTCTCTT 460

QY 540 CCGACTAA 547

Db 461 CTGATTAA 468

RESULT 14

US-09-929-918-3

; Sequence 3, Application US/09929918
; Patent No. 6773899
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.

; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
; FILE REFERENCE: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-929-918-3

Query Match 45.1%; Score 284; DB 4; Length 468;

Best Local Similarity 79.0%; Pred. No. 3e-77;
Matches 338; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAACCCAAAGTCTTCTTACTCGAGTAACG 179

Db 41 AGAAGTTTAACTTCGCGCCGGGAATTACAAAACCCAAAGTCTTCTTACTCGAGTAACG 100

QY 180 GAGGACATCTTCGGAATTCGCCAGATGGCACAGTAGATGGGCTCGGATCGCTCGG 239

Db 101 GGGGCCACTTCTCGAGGATCTTCGGATGGCACAGTAGATGGGCAAGGACAGGAGCG 160

QY 240 ACCAGCACATTCAGCTGCAACTCTCGCGCGAAAGCGTTGGAGAGGTCTATATCAAGTCA 299

Db 161 ACCAGCACATTCAGCTGCAACTCAGTGGCGGAAGCGTGGGGAGGTGTATATAAGAGTA 220

QY 300 CGGAGACTGGCGAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG 359

Db 221 CCGAGACTGGCGAGTACCTTGCCATGGACACCGAGCGGCTTTTATACGGCTCACAGACAC 280

QY 360 CTAAAGGAAGTCTGTGTTCTAGAAAGACTAGAGAAACCATTTACAAACGTACATAT 419

Db 281 CAAATGAGGAATGTTGTTCTGGAAGGCTGGAGGAGAACCATTTACAAACCTATATAT 340

QY 420 CGAAAAAATCATGCAGAGAAAGTGGTTTGTAGGCTTAAAAAATGTTCTCTGTAGC 479

Db 341 CCAAGAGCATGCAGAGAGAAATGTTGTTGGCTCAAGAGAAATGGGAGCTGCAAC 400

QY 480 GTGGACACCGAGTACTATAGGCCAAAGGCTATCTGTCTGCGCACTACCAAGTACGCT 539

Db 401 GCGGTCTCGGACTACTATGGCCAGAAAGCAATCTGTGTTCTCCCGCTGCCAGTCTCTT 460

QY 540 CCGACTAA 547

Db 461 CTGATTAA 468

RESULT 15

5437995-1

; Patent No. 5437995
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;
; SENDO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANIBODY AGAINST AN ACIDIC
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/26,257
; FILING DATE: 04-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588,343
; FILING DATE: 26-SEP-1990
; SEQ ID NO:1:
; LENGTH: 450
5437995-1

Query Match 38.4%; Score 242; DB 6; Length 450;

Best Local Similarity 79.1%; Pred. No. 2.5e-64;

		Matches	337;	Conservative	0;	Mismatches	85;	Indels	4;	Gaps	4;
Qy	122	ATGTTTAACTTCCGCGCGGGAATTACAAAAACCCAAAGCTTCTTTACTGCGAGTAACGGA	181								
Db	14	ATGTTTAAATCTGCTCCCGGGAATTACAAAGAGCCCAAACTCCTCTACTGCGCAACCGG	73								
Qy	182	GGACACTTCTCGGAATTCTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGAC	241								
Db	74	GGCCACTTCTGAGGATTTCTCGGATGGCAAGTGGATGGGACAAAGGA-CAGGACGAC	132								
Qy	242	CAGCACATTGAGTGCAGCTCTCGGCGGAAAGCGTTGGAGAGTCTATATCAAGTCGACG	301								
Db	133	CAGCACATTGAGTGCAGCTCTCGGCGGAAAGCGTTGGAGAGTCTATATCAAGTAC	192								
Qy	302	GAGACTGGCCAGTACCTTGGCATGGACACCGATGGGCTTCTGTATGGCTCACAGAGCCT	361								
Db	193	GAGACTGGCCAGTA-CTTGGCAATGACACCGACGGCTTTTATACGGCTCACAGACACCA	251								
Qy	362	AACGAAGAATGCTTGTCTTAGAAAGACTAGAAAGAAAAACATTACAAACGTCACATATCG	421								
Db	252	AATGAGGAATGTTGTCTTGGAAAGCTGGAGAGAACCATTTACAAACCTATATATCC	311								
Qy	422	AAAAAACATGCAGAGAAAGTGGTTTGTAGGCTTTAAAAAAATGGTTCTGTAAAGCT	481								
Db	312	AAGAAGCATGCAGAGAAAGTTCCTTTGTTGGCTCAAGAAGAAATGG-AGCTGCAAAACGC	370								
Qy	482	GGACCAAGGACTCACTATGGCCAAAAGGCTATCTTGTCTGCGCACTACGAGTACCTCC	541								
Db	371	GGTCTCGGACTCACTAT-GCCAGAAAGCAATCTTGTCTTCCCTCCCTGCCAGTCTCTTCT	429								
Qy	542	GAATAA	547								
Db	430	GATTAA	435								

Search completed: June 17, 2005, 02:31:24
Job time : 167 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2005, 00:13:55 ; Search time 2869 seconds
(without alignments)
8358.484 Million cell updates/sec

Title: US-10-649-480A-6
Perfect score: 630
Sequence: 1 gcgtagagatcgagatctc.....ctgagatcgggtgctaaca 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_hic1:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.4	45.3	534	1 AI590078	tm58c01.x
2	285.4	45.3	821	4 BI598390	603250094
3	285.4	45.3	1014	4 BM809005	AGENCOURT
4	285.4	45.3	1098	5 BX444567	BX444567
5	283	44.9	625	7 CV030767	9975 Full
6	275.2	43.7	1057	5 BQ067949	AGENCOURT
7	275	43.7	508	9 CG633840	OST353987
8	275	43.7	635	7 CK624469	miz1e12.y
9	275	43.7	855	4 BI331990	602984393
10	275	43.7	3404	3 AK035330	Mus muscu
11	274.4	43.6	878	4 BI753845	603027526
12	274.2	43.5	472	1 AI077609	ov26d02.8
13	273.4	43.4	663	1 AI119291	ue95c07.y
14	264.4	42.0	714	4 BG706412	602663744
15	264	41.9	832	4 BI869731	603393620
16	261.2	41.5	689	1 AI663400	uk32d07.y
17	261	41.4	843	4 BI692283	603342751
18	261	41.4	2206	3 BC027001	Mus muscu
19	260.6	41.4	526	9 CG565930	OST191133
20	260.6	41.4	631	2 BB627624	BB627624
21	256.4	40.7	809	7 CO420661	GGEZHC101
22	249.6	39.6	461	4 BF956865	RC1-NN023
23	233.2	37.0	813	2 BF532970	602073491
24	228.4	36.3	611	5 BU840197	AGENCOURT

25	209.6	33.3	546	7	CR533323	CR533323	DKF2p459M
26	208.2	33.0	503	2	BF442355	BF442355	259038 WA
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c 28	203.4	32.3	750	5	BU627243	BU627243	UI-H-FG0-
29	203.2	32.3	543	1	AA261582	AA261582	mz87c09.r
30	203	32.2	395	6	CB773841	CB773841	AMGNNUC:S
31	194.8	30.9	529	9	CG629018	CG629018	OST340697
c 32	190.8	30.3	429	2	AW531286	AW531286	UI-R-C4-a
33	189	30.3	288	6	CB710781	CB710781	AMGNNUC:N
34	188.6	29.9	469	2	AW259195	AW259195	um89f09.Y
35	186.4	28.6	926	6	CD253719	CD253719	AGENCOURT
36	182.2	28.9	570	4	BM364189	BM364189	BS3000090
37	180	28.6	543	7	CR537204	CR537204	DKF2p459K
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39	171	27.1	898	6	CD301410	CD301410	AGENCOURT
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41	167.8	26.6	522	6	CD701495	CD701495	EST18019
c 42	164.4	26.1	458	1	AA594274	AA594274	nl90g01.8
43	161.6	25.7	677	7	CV067690	CV067690	Le_mk0.37
44	159.6	25.3	406	6	CB807695	CB807695	AMGNNUC:S
45	159.4	25.3	226	4	BI423446	BI423446	CM85 Deer

ALIGNMENTS

RESULT 1
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LOCUS tm58c01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162304 3',
DEFINITION similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1
(HUMAN);, mRNA sequence.
ACCESSION AI590078
VERSION AI590078.1 GI:4599126
KEYWORDS .EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 534)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 736 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2162304"
/issue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn25"
/note="Organ: Brain; Vector: pTTT3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCAATCTGAAGTGGAGCGGCATAGTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaído."

ORIGIN

```
Query Match      45.3%; Score 285.4; DB 1; Length 534;
Best Local Similarity 78.9%; Pred. No. 6e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTTCTTTACTGCAGTAACG 179
    |||||
Db 464 AGAAGTTTAACTTCGCTCCAGGGAATTACAGAGCCCAACTCTCTACTGTAGCAACG 405

QY 180 GAGGACACTTCCTCGGAATTTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
    |||||
Db 404 GGGGCCACTTCCTGAGGATCCTTCGGATGGCACAGTGGTGGCAAGGGACAGGAGCG 345

QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAGGTTGGAGAGGCTCTATATCAAGTCGA 299
    |||||
Db 344 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAGGTTGGGAGGAGGTGTATATAAAGATA 285

QY 300 CGGAGACTGGCCAGTACCTTGCATGGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG 359
    |||||
Db 284 CCGAGCTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACAC 225

QY 360 CTAAAGGAATGCTTGTGTTCTAGAAAGACTAGAGAAACCAATTACAGAGTACATAT 419
    |||||
Db 224 CAAATGAGGAATGTTTGTCTCGGAAAGGCTGGAGGAGAACCAATTACACACCTATATAT 165

QY 420 CGAAAAACATCGACAGAGAACTGGTTGTAGGCTTTAAAAAATGTTCTCTGTAAGC 479
    |||||
Db 164 CCAAGAGCATCGACAGAGAAATGGTTGTGTGGCTCAAGAAGAAATGGGAGCTGCAAC 105

QY 480 GTGGACACGAGTCACTATGCGCAAAAGGCTATCTTGTCTGCGCACTACCAAGTGA 539
    |||||
Db 104 GGGTCTCGGACTCACTATGCGCAAAAGGCTATCTTGTCTGCGCACTACCAAGTGA 45

QY 540 CCGACTAAGGA 550
    |||||
Db 44 CTGATTAAAGA 34
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RESULT 2
BI598390
LOCUS      603250094F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302030 5',
DEFINITION mRNA sequence.
ACCESSION BI598390
VERSION    BI598390.1 GI:15491329
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 821)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11764 row: k column: 23
            High quality sequence stop: 777.
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FEATURES
source
1..821

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5302030"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site: BamHI; Site_2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."
```

ORIGIN

```
Query Match      45.3%; Score 285.4; DB 4; Length 821;
Best Local Similarity 78.9%; Pred. No. 6.7e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTTCTTTACTGCAGTAACG 179
    |||||
Db 190 AGAAGTTTAACTTCGCTCCAGGGAATTACAGAGCCCAACTCTCTACTGTAGCAACG 249

QY 180 GAGGACACTTCCTCGGAATTTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
    |||||
Db 250 GGGGCCACTTCCTGAGGATCCTTCGGATGGCACAGTGGTGGCAAGGGACAGGAGCG 309

QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAGGTTGGAGAGGCTCTATATCAAGTCGA 299
    |||||
Db 310 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAGGTTGGGAGGAGGTGTATAAAGATA 369

QY 300 CGGAGACTGGCCAGTACCTTGCATGGGACACCGATGGGCTTCTGTATGGCTCACAGAGCG 359
    |||||
Db 370 CCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACAC 429

QY 360 CTAAAGGAATGCTTGTGTTCTAGAAAGACTAGAGAAACCAATTACAGAGTACATAT 419
    |||||
Db 430 CAAATGAGGAATGTTTGTCTCGGAAAGGCTGGAGGAGAACCAATTACACACCTATATAT 489

QY 420 CGAAAAACATCGACAGAGAACTGGTTGTAGGCTTTAAAAAATGTTCTCTGTAAGC 479
    |||||
Db 490 CCAAGAGCATCGACAGAGAAATGGTTGTGTGGCTCAAGAAGAAATGGGAGCTGCAAC 549

QY 480 GTGGACACGAGTCACTATGCGCAAAAGGCTATCTTGTCTGCGCACTACCAAGTGA 539
    |||||
Db 550 GGGTCTCGGACTCACTATGCGCAAAAGGCTATCTTGTCTGCGCACTACCAAGTGA 609

QY 540 CCGACTAAGGA 550
    |||||
Db 610 CTGATTAAAGA 620
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```
RESULT 3
BI598390
LOCUS      6617747 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:573445
DEFINITION 5', mRNA sequence.
ACCESSION BI598390
VERSION    BI598390.1 GI:19125828
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1014)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12739 row: m column: 06
High quality sequence stop: 637.
Location/Qualifiers
1. .1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5734445"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 124"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcorV
(destroyed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dr primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

FEATURES

source

ORIGIN

Query Match 45.3%; Score 285.4; DB 4; Length 1014;
Best Local Similarity 78.9%; Pred. No. 7.1e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 120 ATATGTTTAACTTCGCGCGGAATTACAAAAACCCAGCTTCTTTACTGCAGTAACG 179
Db 223 AGAAGTTTAACTTCGCGCGGAATTACAAAAACCCAGCTTCTTTACTGCAGTAACG 282
QY 180 GAGGACATCTCCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGCTCGG 239
Db 283 GGGGCCACTTCCTGAGGATCTTCGGATGGCACAGTAGATGGGAGGCAAGGACAGGAGCG 342
QY 240 ACCAGACATTCAGCTGCAACTCTCGGCCCAAGACGTTGGAGAGGTCTATATCAAGTCGA 299
Db 343 ACCAGACATTCAGCTGCACTCAGTGGGGAAGCGTTGGGGAGGTCTATATAAGAGTA 402
QY 300 CGGAGACTGGCCAGTACCTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACGC 359
Db 403 CGGAGACTGGCCAGTACTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACGC 462
QY 360 CTAAACGAGATGCTTGTCTTCTAGAGACTAGAGAAACCATTAACAACCGTACATAT 419
Db 463 CAAATGAGGAATGTTTGTCTCGAAGGCTGGAGGAGAACCATTAACAACCGTACATAT 522
QY 420 CGAAAAACATGACAGAGAAGAACTGGTTTCTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
Db 523 CCAGAGAGCATGACAGAGAAGAAATGGTTTGTGGCTTCAAGAGAATGGGAGCTGCAAC 582
QY 480 GTGGACACCGACTCACTATGGCCAAAGGCTATCTTGTCTTCCGCCACTACCGATGAGCT 539
Db 583 CGGCTCTCGGACTCACTATGGCCAAAGGCTATCTTGTCTTCCGCCACTACCGATGAGCT 642
QY 540 CCGACTAAGGA 550
Db 643 CTGATTAAAGA 653

RESULT 4

BX444567
LOCUS BX444567 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN003YP16 5-PRIME, mRNA sequence.
ACCESSION BX444567
VERSION BX444567.2 GI:47009158

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1098)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30780253.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcorV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3201.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DN003DH08QP1&c=3201.r.

Location/Qualifiers

1. .1098

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DN003YP16"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcorV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Query Match 45.3%; Score 285.4; DB 5; Length 1098;
Best Local Similarity 78.9%; Pred. No. 7.2e-74;
Matches 340; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 120 ATATGTTTAACTTCGCGCGGAATTACAAAAACCCAGCTTCTTTACTGCAGTAACG 179
Db 151 AGAAGTTTAACTTCGCGCGGAATTACAAAAACCCAGCTTCTTTACTGCAGTAACG 210
QY 180 GAGGACATCTCCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGCTCGG 239
Db 211 GGGGCCACTTCCTGAGGATCTTCGGATGGCACAGTAGATGGGCAAGGACAGGAGCG 270
QY 240 ACCAGACATTCAGCTGCAACTCTCGGCCCAAGACGTTGGAGAGGTCTATATCAAGTCGA 299
Db 271 ACCAGACATTCAGCTGCACTCAGTGGGGAAGCGTTGGGGAGGTCTATATAAGAGTA 330
QY 300 CGGAGACTGGCCAGTACCTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACGC 359
Db 331 CGGAGACTGGCCAGTACTTGGCCATGGACACCGATGGGCTTCTGTATGGCTCAGACGC 390
QY 360 CTAAACGAGATGCTTGTCTTCTAGAAAGACTAGAGAAACCATTAACAACCGTACATAT 419
Db 391 CAAATGAGGAATGTTTGTCTCGAAGGCTGGAGGAGAACCATTAACAACCGTACATAT 450
QY 420 CGAAAAACATGACAGAGAAGAACTGGTTTCTAGGCTTTAAAAAATGGTTCTCTGTAAGC 479
Db 451 CCAGAGAGCATGACAGAGAAGAAATGGTTTGTGGCTTCAAGAGAATGGGAGCTGCAAC 510
QY 480 GTGGACACCGACTCACTATGGCCAAAGGCTATCTTGTCTTCCGCCACTACCGATGAGCT 539
Db 511 CGGCTCTCGGACTCACTATGGCCAAAGGCTATCTTGTCTTCCGCCACTACCGATGAGCT 570
QY 540 CCGACTAAGGA 550
Db 571 CTGATTAAAGA 581

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RESULT 5
CV030767
LOCUS          CV030767          625 bp      mRNA      linear      EST 20-AUG-2004
DEFINITION    9975 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC032697, mRNA sequence.
ACCESSION    CV030767
VERSION      CV030767.1  GI:51489048
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 625)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,D., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGGCTGAAGGGGAATCAC
BACKWARD: TAATCAGAAGACTGCGAGG
Insert Length: 625 Std Error: 44.00
Place: 11032 row: 09 column: F
Seq primer: ACTGCCGTCGTGTACACACGTCGTGACTGGGAAAC
High quality sequence start: 100
High quality sequence stop: 624
POLVA=No.

FEATURES             Location/Qualifiers
     source           1..625
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     tissue_type="mixed"
     clone_libs="Full Length cDNA from the Mammalian Gene Collection"
     note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN
Query Match          44.9%; Score 283; DB 7; Length 625;
Best Local Similarity 78.9%; Pred. No. 3 3e-73;
Matches 337; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 120 ATATGTTTAACCTTCGCCCGGAATTACAAAAACCCAAAGTCTTTTACTCAGTAACG 179
Db 41 AGAAGTTTAATCTGCTCCAGGGAATTACAAGAAGCCCAACTCTCTACTGTAGCAACG 100
QY 180 GAGGACATCTCTCGGAATCTCCAGATGGGCACAGTAGATCGGATCGGATCGCTCG 239
Db 101 GGGGGCCATCTCTGAGGATCTCTCCGATGGGCACAGTAGATCGGACAGGAGCG 160
QY 240 ACCAGCACATTCAGCTGCAACTCTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
Db 161 ACCAGCACATTCAGCTGCAAGCTCAGTCGCGGAAGCGTGGGGAGGTGTATATAAGAGTA 220

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QY 300 CGGAGACTGGCCAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCAGAGCGC 359
Db 221 CCGAGACTGGCCAGTACTTGCCATGGACACCGACCGGCTTTTATACGGCTCAGAGCAC 280
QY 360 CTAACGAGAGTCTGTTTCTAGAAAGACTAGAGAAACCATTAACAACAGTACATAT 419
Db 281 CAAATGAGGAATGTTTCTCTGGAAGGCTGGAGGAGAACATTTACAAACCTATATAT 340
QY 420 CGAAAAAATCATGCAGAGAAACTGGTTTGTAGGCTTTAAAAAAAATGGTTCCTGTAAAGC 479
Db 341 CCAAGAGCATGCAGAGAGAAATTTGTTTGTGGCTCAAGAAGATGGGAGCTGCAAAAC 400
QY 480 GTGACCACGAGCTACATATGCGCAAAAGGCTATCTTGTTCCTGCCATACAGTGAGCT 539
Db 401 CGGTCCTCGGACTCACTATGCGCAGAAAGCAATCTTGTTTCTCCCTCCGCTCTCTT 460
QY 540 CCGACTA 546
Db 461 CTGATTA 467

RESULT 6
BO067949
LOCUS          BO067949          1057 bp      mRNA      linear      EST 02-APR-2002
DEFINITION    AGENCOURT_6792377 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5768943
5', mRNA sequence.
ACCESSION    BO067949
VERSION      BO067949.1  GI:19896995
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1057)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12829 row: j column: 16
High quality sequence stop: 470.

FEATURES             Location/Qualifiers
     source           1..1057
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clones="IMAGE:5768943"
     lab_host="DH10B"
     clone_libs="NIH_MGC_121"
     note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN
Query Match          43.7%; Score 275.2; DB 5; Length 1057;
Best Local Similarity 79.7%; Pred. No. 8.1e-71;
Matches 325; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

```


QY	120	ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTCTTTTACTGCAGTAACG	179
Db	181	AGAAAGTTTAACTTCGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACG	240
QY	180	GAGGACATCTTCCTCGGAAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCGG	239
Db	241	GGGGCCACTTCCTGAGGATCCTTCGGATGGCACAGTGGTGGCAAGGGACAGGAGCG	300
QY	240	ACCAGACATTCAGCTGGAACCTTCGGCCGAAGCGTTGGAGAGGTCTATATCAAGTCGA	299
Db	301	ACCAGACATTCAGCTGCGACTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAGAGTA	360
QY	300	CGGAGACTGCGCAGTACCTTGGCATGGACACCGATGGGCTTCGTATGGCTCACAGACG	359
Db	361	CGGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGAC	420
QY	360	CTAACCGAAGAATGCTTGTCTAGAAAGACTAGAGAAAAACCATTAACAACGTCATAT	419
Db	421	CAAAATGAGGAATGTTGTTCTCGGAAGGCTGGAGGAGAACCATTAACAACCTATATAT	480
QY	420	CGAAAAAATGAGAGAGAACTGTTGTAGGCTTTAAAAAATGTTTCTGTAAAC	479
Db	481	CCAAGAAGCATGCAGAGAAAGATTGTTGTTGGCCCTCAAGAAGAATGGGAGTCGAAC	540
QY	480	GTGACACCGGACTCACTATGGCCAAAGGCTATCTTGTTCCTGCCAC	527
Db	541	CGGGTCTCGGACTACTATGGCCAGAAAGCAATCTTGTTCCTCCCC	588

RESULT 7

CG633840

LOCUS

OST353987 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST353987, mRNA sequence.

ACCESSION

CG633840

VERSION

CG633840.1

GI:37457689

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 508)

AUTHORS

Zambrowicz,B.P., Ahuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slijkenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT

Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

Source

1..508

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST353987"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 43.7%; Score 275; DB 9; Length 508;

Best Local Similarity 77.8%; Pred. No. 7.7e-71;

Matches	332;	Conservative	0;	Mismatches	95;	Indels	0;	Gaps	0;
QY	120	ATATGTTTAACTTCGCGCCGGGAATTACAAAAACCCCAAGCTTCTTTTACTGCAGTAACG	179						
Db	79	AGAGGTTTCAACTTGCCTCTAGGAAACTACAAAAGGCCAAACTGTCTACTGCAGCAACG	138						
QY	180	GAGGACATCTCTCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG	239						
Db	139	GGGGCCACTTCCTGAGGATCCTTCCTGATGGCACCGTGGATGGGACAAAGGGACAGGAGCG	198						
QY	240	ACCAGACATTCAGCTGCAACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGA	299						
Db	199	ACCAGACATTCAGCTGCGACTCAGTGGCGAAAGTCGGCGGAAAGTGTATATAAAGGTA	258						
QY	300	CGGAGACTGGCCAGTACCTTGCCATGGACACCGATGGGCTTCTGTATGGCTCACAGACG	359						
Db	259	CGGAGACCGGCCAGTACTTGGCCATGGACACCGAAGGGCTTTTATACGGCTCGAGACAC	318						
QY	360	CTAACGGAAGAATGCTTGTCTTAGAAAGACTAGAGAAAAACCATTAACAACGTCATAT	419						
Db	319	CAAAATGAGGAATGCTGTTCTCTGGAAAGGCTGGAAGAAACCATTAACAACCTACACT	378						
QY	420	CGAAAAAATGAGAGAGAACTGTTTGTAGGCTTTAAAAAATGTTTCTGTAAAC	479						
Db	379	CCAAGAAGCATGCGGAGAAAGACTGTTTGTGGGCTCTAAGAAGAAACGGGAGCTGTAACG	438						
QY	480	GTGCAACCGGACTCACTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCAAGTGAGCT	539						
Db	439	CGGGTCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTCGCCCTCCCGGTGTCTT	498						
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Db	499	CTGACTA 505							

/note="Organ: Eye; Vector: pSport1; 64ug total RNA was extracted from 200 adult male mouse RBE/choroids. A directionally cloned cDNA library in the pSPORT1 vector(Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTTAGATCGGCGGCCCT(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 43.7%; Score 275; DB 7; Length 635;
Best Local Similarity 77.8%; Pred. No. 8.2e-71;
Matches 332; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCGGGAATTACAAAAACCCAGCTTCTTTACTGCACTAAGC 179
DB 184 AGAGGTTCAACCTGCTCTAGGAACTACAAAAAGCCCAAACTGCTCTACTGCAACAACG 243
QY 180 GAGGACACTTCTCGGAATTTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
DB 244 GGGGCCACTTCTTGAGGATCTCTCTGATGGCACCGTGGATGGGACAGGACAGGAGG 303
QY 240 ACCAGCAATTCAGCTGCNACTCTCGCGCAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 304 ACCAGCACATTCAGCTGCAGCTCAGTGGCGAAAGTGGCGGCAAGTGTATATAAAGGTA 363
QY 300 CGGAGCTGGCCAGTACCTTGCATGACACCGATGGGCTTCTGTATGGCTCAGACAGCG 359
DB 364 CGGAGCGCGGCGAGTCTGGCCATGGACACCGAAGGGCTTTTATACGGCTCGCAGACAC 423
QY 360 CTAACGAGAACTGTTGTTCTAGAAAGACTAGAAAGAAACCATTAACAACGATACATAT 419
DB 424 CAATGAGGAAATGCTGTTCTGGAAGGCTGGAGAAACCATTAACAACCTTACACT 483
QY 420 CGAAAAACATCGAGAGAACTGGTTGTAGGCTTTAAAAAATGTTCTCTGTAAGC 479
DB 484 CCAAGAAGCATCGGAGAAGAACTGGTTGTGGGCTCAAGAAGAACGGGAGCTGTAAGC 543
QY 480 GTGGACCGGACTCACTATGGCCAAAGGCTATCTTGTCTGCGCACTACCACTGAGCT 539
DB 544 GCGGTCTCGGACTCACTATGGCCGAAAGCCATCTTGTCTGCCCCCTCCCGGTGCTT 603
QY 540 CCGACTA 546
DB 604 CTGACTA 610

RESULT 9
BI331990
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI331990 855 bp mRNA linear EST 30-JUL-2001
602984393Fi NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5137246 5',
mRNA sequence.
BI331990
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11337 row: i column: 23
High quality sequence stop: 752.

FEATURES

source
1..855
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5137246"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 43.7%; Score 275; DB 4; Length 855;
Best Local Similarity 77.8%; Pred. No. 8.8e-71;
Matches 332; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 120 ATATGTTTAACTTCGCGCGGGAATTACAAAAACCCAGCTTCTTTACTGCACTAAGC 179
DB 235 AGAGGTTCAACCTGCTCTAGGAACTACAAAAAGCCCAAACTGCTCTACTGCAACAACG 294
QY 180 GAGGACACTTCTCGGAATTTCTGCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
DB 295 GGGGCCACTTCTTGAGGATCTCTCTGATGGCACCGTGGATGGGACAGGACAGGAGCG 354
QY 240 ACCAGCAATTCAGCTGCNACTCTCGCGCAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
DB 355 ACCAGCACATTCAGCTGCAGCTCAGTGGCGAAAGTGGCGGCAAGTGTATATAAAGGTA 414
QY 300 CGGAGCTGGCCAGTACCTTGCATGACACCGATGGGCTTCTGTATGGCTCAGACAGCG 359
DB 415 CGGAGACCGGCGAGTCTTGGCCATGGACACCGAAGGGCTTTTATACGGCTCGCAGACAC 474
QY 360 CTAACGAGAACTGCTGTTCTAGAAAGACTAGAAAGAAACCATTAACAACGATACATAT 419
DB 475 CAATGAGGAAATGCTGTTCTGGAAGGCTGGAGAAACCATTAACAACCTTACACT 534
QY 420 CGAAAAACATCGCAGAGAACTGGTTGTAGGCTTTAAAAAATGTTCTCTGTAAGC 479
DB 535 CCAAGAAGCATCGGAGAAGAACTGGTTGTGGGCTCAAGAAGAACGGGAGCTGTAAGC 594
QY 480 GTGGACCGGACTCACTATGGCCAAAGGCTATCTTGTCTGCGCACTACCACTGAGCT 539
DB 595 GCGGTCTCGGACTCACTATGGCCGAAAGCCATCTTGTCTGCCCCCTCCCGGTGCTT 654
QY 540 CCGACTA 546
DB 655 CTGACTA 661

RESULT 10
AK035330
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AK035330 3404 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:953001822 product:fibroblast growth factor
1, full insert sequence.
AK035330
AK035330.1 GI:26330609
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1495 row: d column: 08
High quality sequence stop: 703.
Location/Qualifiers
1. .878
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197783"
/lab_host="DH10B"
/clone_lib="NIH MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

SOURCE ORGANISM

Homo sapiens (human)
Homo sapiens

REFERENCE

1 (bases 1 to 472)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 649 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .472
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1666947"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts_NbHSP"
/note="vector: pT7T3D (pharmacia) with a modified polylinker V.TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dtr) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 43.5%; Score 274.2; DB 1; Length 472;
Best Local Similarity 77.3%; Pred. No. 1.3e-70;
Matches 333; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy	120	ATATGTTTAACTTCGCGCGGAATTACAAAACCAAGCTTCTTTACTGCAGTAACG	179
Db	461	AGAAAGTTTAACTTCGCGCGGAATTACAAAACCAAGCTTCTTTACTGTAGCAACG	402
Qy	180	GAGGACACTTCCTCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG	239
Db	401	GGGCTCACTTCCTGAGCGATCTTCGGATGGCACAGTGGATGGAAAGGACAGGAGCG	342
Qy	240	ACGAGCAATTCAGCTGCAACTCTCGGCGGAAGCGTTGGAGAGGTCTATATCAAGTCGA	299
Db	341	ACCAGCAATTCAGCTGCACTAGTCGGAAGCGTGGGAGGTGTATATAAGAGTA	282
Qy	300	CGGAGCTGGCCAGTACCTTCCCATGGACACCGATGGCTTCTGTATGGCTCACAGAGC	359
Db	281	CCGAGACTTGGCAGTACTTGGCCATGGACACCGACGGGCTTTATACGGCTCACAGAC	222
Qy	360	CTAACGAAGATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCACATAT	419
Db	221	CAATGAGGAATTTTGTCTCGGAGGGCTGGAGGAGNACCATTAACAACCTATATAT	162
Qy	420	CGAAAAACATGCAGAGAGAACTGGTTTGTAGCCCTTAAAAAATGGTTCCTGTGAAGC	479
Db	161	CCAAGAAGCATGCAGAGAGAAATTTGGTTTGTGGCCCTCAAGAAGATGGGAGCTGCAAC	102
Qy	480	GTGGACCAACGACCTACCTATGGCCAAAGGCTATCTTGTTCCTCCCACTACCACTGAGCT	539
Db	101	CGGTGCTTCGGACTCCTATATGGCCAAAGCAATCTTGTTCCTCCCTGCGAGTCTCTT	42
Qy	540	CCGACTAAGGA	550

FEATURES
source

ORIGIN

Query Match 43.6%; Score 274.4; DB 4; Length 878;
Best Local Similarity 78.7%; Pred. No. 1.3e-70;
Matches 340; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
Qy 120 ATATGTTTAACTTCGCGCGGAATTACAAAACCAAGCTTCTTTACTGCAGTAAC 178
Db 157 AGAAGTTTAACTTCGCGCGGAATTACAAAACCAAGCTTCTTTACTGTAGCAAC 216
Qy 179 GAGGACACTTCCTCGGAATTCGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCC 238
Db 217 GGGGCCACTTCCTGAGGATCTTCGGATGGCACAGTGGTGGGACAGGAGGAGC 276
Qy 239 GACGAGCAATTCAGCTGCAACTCTCGGCGGAAGCGTTGGAGAGGTCTATATCAAGTCG 298
Db 277 GACGAGCAATTCAGCTGCACTAGTCGGAAGCGTGGGAGGTGTATATAAGAGT 336
Qy 299 ACGGAGCTGGCCAGTACCTTCCCATGGACAGGATGGCTTCTGTATGGCTCACAGAGC 358
Db 337 ACCGAGCTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACA 396
Qy 359 CCTAACGAAGATGCTTGTCTAGAAAGACTAGAAAGAAACCATTAACAACGTCACATA 418
Db 397 CCATATGAGGAATGTTGTCTCGGAAAGCTGGAGGAGNACCATTAACAACCTATATA 456
Qy 419 TCGAAAAACATGCAGAGAGAACTGGTTTGTAGGCTTTAAAAAATGGTTCCTGTGAAG 478
Db 457 TCCAAAGACATGCAGAGAGAAATCGTTTGTAGGCCTCAAGAAGATGGGAGCTGCAAA 516
Qy 479 CGTGGACCAACGACCTACCTATGGCCAAAGGCTATCTTGTTCCTGCCACTACCACTGAGC 538
Db 517 CGGTGCTTCGGACTCCTATATGGCCAAAGCAATCTTGTATCTCCCCCTGCCAGTCTCT 576
Qy 539 TCCGACTAAGGA 550
Db 577 TCTGATTAAAGA 588

RESULT 12
AI077609/c
LOCUS
DEFINITION
AI077609 472 bp mRNA linear EST 24-SEP-1998
oy26d02.s1 Soares senescent fibroblasts NbHSP Homo sapiens CDNA
clone IMAGE:1666947 3' similar to gb:MI3361 HEPARIN-BINDING GROWTH
FACTOR PRECURSOR 1 (HUMAN) ; mRNA sequence.
ACCESSION
AI077609
VERSION
AI077609.1 GI:3412017
KEYWORDS
EST.

Db 41 CTGATTAAAGA 31

RESULT 13
AII19291
LOCUS
DEFINITION
u95c07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1498860 5', similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR
PRECURSOR 1 (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenger, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:936464

Seq primer: custom primer used
High quality sequence stop: 527.

FEATURES
source
1. .663
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1498860"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/clone_lib="Sugano mouse embryo mewa"
/notes="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGCTGGC and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN
Query Match 43.4%; Score 273.4; DB 1; Length 663;
Best Local Similarity 77.5%; Pred. No. 2.5e-70;
Matches 331; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 120 ATATGTTTAACTTCGCGCGGGGAATTAACAAAACCAAGCTCTTTTACTGCAAGTAAACG 179
Db 216 AGAGTTCAACCTCGCTCTAGGAACACTACAAAAGCCAACTGCTCTACTGCAAGTAAACG 275
Qy 180 GAGGACACTCTCTCGCAATTTCTGCAGATGCGACAGTAGTAGGCACTTCGCGACTGCTCCG 239
Db 276 GGGGCCACTCTTCTGAGGATCTCTCTGATGCGACCGCTGGATGGGCAAGGACGAGGAGCG 335

Qy 240 ACCAGCACATTCACTCAGCTCCTCGCGCGAAACGCTTGGAGAGGCTTATATCAAGTGA 299
Db 336 ACCAGCACATTCACTCAGCTCCTCGCGCGAAAGTGGCGGCGAAGTGTATATAAAGGCTA 395
Qy 300 CGGAGACTGGCCAGTACCTTCCCATGGACACCGATGGCTTCTGTATGGCTCACAGACGC 359
Db 396 CGGAGACCGCGCAGTACTTGGCCATGGACACCGAAGGCTTTTATACGGCTCGCAGACAC 455
Qy 360 CTAACGAGAATGCTGTGTTCTAGAAAGACTAGAAAGAAACCATTTACAAACGTCACATAT 419
Db 456 CAATAGAGAAATGCTGCTCTCTGGAAGGCTGGAGAAGAAACCATTTATACACTTACACCT 515
Qy 420 CGAAAAAATCATCGAGAGAAAGTGGTTTGTAGCCCTTAAAAAATGGTTCCTGTAAGC 479
Db 516 CCAAGAACATCGCGAGAAAGTGGTTTGTGGGCTCAAGAAGAAACGGAGCTGTAAAGC 575
Qy 480 GTGACACCGGACTCAGTATGCGCAAGGCTATCTTGTCTCCACTACAGTGAGCT 539
Db 576 GCGGTCTCTCGACTCAGTATGCGCAAGAAAGCATCTTGTCTGCCCTCCCGGTGCTT 635
Qy 540 CCGACTA 546
Db 636 CTGACTA 642

RESULT 14
BG706412
LOCUS
DEFINITION
602669744F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792378 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BG706412
BG706412.1 GI:13981735
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1. (bases 1 to 714)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10670 row: h column: 11
High quality sequence stop: 710.
Location/Qualifiers
1. .714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792378"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH MGC 96"
/notes="Organ: brain; Vector: pBluescriptR (modified pluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTN-3', size-selected for average insert size 2.3 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.0%; Score 264.4; DB 4; Length 714;
 Best Local Similarity 78.6%; Pred. No. 1.2e-67;
 Matches 316; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 126 TTAACCTTCGCGCGGAATTACAAAACCAAGCTTCTTACCTGACAGTACGAGGAC 185
 DB 195 TTTAATCTCGCTCCAGGAATTACAAAGCCCAAACTCTCTACTGTAGCAACGGGGGCC 254

QY 186 ACTTCTCGGAATCTTCCAGATGGCACAGTAGATGGGACTCGCATCGCTCCGACCCAGC 245
 DB 255 ACTTCTGAGGATCTTCCGGATGGCACAGTGGATGGGACAGGACGACGACCCAGC 314

QY 246 ACATTGAGTCAATCTCTCGCGGAAAGCGTTGGAGAGTCTATATCAAGTGCAGCGAGA 305
 DB 315 ACATTGAGTGCAGTCTAGTGGGAAAGCGTTGGGAGGTTATATAAGAGTACCGAGA 374

QY 306 CTGGCCAGTACCTTGCATGGACCGATGGGCTTCTGTATGGCTCACAGCGCCTAAGC 365
 DB 375 CTGGCCAGTACCTTGCATGGACCGATGGGCTTCTGTATGGCTCACAGCGCCTAAGC 434

QY 366 AAGAAATGCTTGTCTTAGAAGACTAGAAAGAAACCATTTACACACGTCATATCGAAAA 425
 DB 435 AGGAATGTTGTTCTTGGAAAGCTGGAGGAGAACCATTTACACACCTATATCCAAGA 494

QY 426 ACATGACAGAGAAAGCTGTTGTAGGCTTAAAGAAATGGTTCCTGTAGCGTGGAC 485
 DB 495 AGCATGACAGAGAAAGTGTGTTGTGGCTCAAGAAAGTGGAGCTGCAAAACCGGTC 554

QY 486 CACGAGTCACTATGGCCAAAGGCTATCTGTCTCTGCCAC 527
 DB 555 CTCGGAATCCTATGGCCAAAGGCTATCTGTCTCTCCCC 596

RESULT 15
 BI869731
 LOCUS 60393620F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403677 5',
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 ACCESSION BI869731
 VERSION BI869731.1 GI:16043404
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12029 row: g column: 06
 High quality sequence stop: 829.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5403677"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_90"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for

full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 41.9%; Score 264; DB 4; Length 832;
 Best Local Similarity 78.7%; Pred. No. 1.7e-67;
 Matches 340; Conservative 0; Mismatches 90; Indels 2; Gaps 2;

QY 120 ATATGTTTAACTTCCCGCGGGAATTACAAAACCAAGCTTCTTACTGCAAGTAAACG 179
 DB 120 AGAAGTTTAACTTCCCGCGGGAATTACAAAAGCCCAAACTCTCTACTGTAGCAACG 179

QY 180 GAGGACACTTCTCGGAATTTCTCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCG 239
 DB 180 GGGGCCACTTCTCGGATCCCTCCGATGGCACAGTGGATGGGACAAAGGACAGGAGCG 239

QY 240 ACCAGCACATTCAGCTCGCACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGA 299
 DB 240 ACCAGCACATTCAGCTCGCACTCTCGGCCGAAAGCGTTGGAGAGGTCTATATAAGAGTA 299

QY 300 CGGAGACTGGCCAGTACCTTGGCCATGGCACCCGATGGGCTTCTGTATGGCTCACAGACG 359
 DB 300 CCGAGACTGGCCAGTACCTTGGCCATGGCACCCGATGGGCTTCTGTATGGCTCACAGACG 359

QY 360 CTAACGAGATGCTTCTTCTAGAAAGACTAGAAAGAAACCATTTACACACGTCATATAT 419
 DB 360 CAAATGAGGAATG-TTGTCTCGAAAGGCTGGAGGAGAACCATTTACACACCTATATAT 418

QY 420 CGAAAAACATGCAGAGAGAACTGGTTTGTAGGCTTTAAAAAAATGGTTCTCTG-TAAG 478
 DB 419 CCAAGAGCATGCAGAGAGAAATTTGGTTTGTGGCTCAAGAGATGGGAGCTGCAAC 478

QY 479 CGTGGACACGAGTCACTATGGCCAAAGGCTATCTTGTCTCGCCACTACCAAGTGAGC 538
 DB 479 CGCGTCTCTCGACTCACTATGGCCAAAGGCTATCTTGTCTCTCCCTGCCAGTCTCT 538

QY 539 TCCGACTAAGGA 550
 DB 539 TCTGATTAAAGA 550

Search completed: June 17, 2005, 02:28:38
 Job time : 2876 secs